

0989575-070504

Gag_AF110965_BW_mod

ATGGGCGCCCGCGCCAGCATCCTGCGCGGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCC
TGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATC
CGCCAGCTGCACCCCGCCCTGCAGACCGGCAGGAGGAGCTGAAGAGCCTGTTCAACACCCG
TGGCCACCCTGTACTGCGTGACGAGAAGATCGAGGTCCGCGACACCAAGGAGGOCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCGCCGAC
AAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAAGCCTGCAGGGCCAGATGGTGACCC
AGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAG
CCCCGAGGTGATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAAC
ACGATGTTGAACACCCTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCA
ACGAGGAGGCCGCCGAGTGGGACCGCGTGACCCCGTGACGCCGGCCCCCATCGCCCCCGG
CCAGATGCGCGAGCCCCCGCGGCAGCGACATCGCCGGCACCACCAGCACCCCTGCAGGAGCAG
ATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTACAAGCGGTGGATCA
TCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCAAGCA
GGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCCTGCGCGCCGAG
CAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCCTGCTGGTGCAAGCGCCAACC
CCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCGCGGCCAGCCTGGAGGAGATGATGAC
CGCCTGCCAGGGCGTGGGCGGGCCCCAGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGC
CAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCATCGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCC
GCCCGAGCCCAACCGCCCCCCCCCGCGAGAGCTTCCGCTTCGAGGAGACCACCCCGGCCA
GAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTGGGCAACGAC
CCCCTGAGCCAGTAA

Figure 1

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ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCC
TGCGCCCCCGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATG
AAGCAGCTGCAGCCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAACACCG
TGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAGGCCGAC
GGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGG
CCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCC
CGAGGTGATCCCCATGTTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACG
ATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACG
AGGAGGCCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCCGGCCCGTGGCCCCCGGCCA
GATGCGCGACCCCCCGCGGCAGCGACATCGCCGGCGGCCACCAGCACCCCTGCAGGAGCAGATC
GCCTGGATGACCAGCAACCCCCCGTGCCCGTGGGCGACATCTACAAGCGGTGGATCATCC
TGGGCCTGAACAAGATCGTGGGATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAGGG
CCCCAAGGAGCCCTTCGCGCACTACGTGGACCGCTTCTTCAAGACCCCTGCGCGCCGAGCAG
GCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCCTGCTGGTGCAGAACGCCAACCCCG
ACTGCAAGACCATCCTGCGCGCTCTCGGCCCGCGGCCACCCCTGGAGGAGATGATGACCGC
CTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAG
GCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCAACGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAGTGGGCAAGGAGGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCCGCCCCGGCAACTTCCTGCAGAACC
GCAGCGAGCCCGCGCCCCCAACCGTGCCACCGCCCCCCCCCGCCGAGAGCTTCCGCTTCGA
GGAGACCACCCCCGCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTG
ACCGCCCTGCGCAGCCTGTTCGGCAGCGGCCCCCTGAGCCAGTAA

Figure 2

Fig. 3

Env_AF110968_C_BW_opt

--> signal peptide (1-81)
ATGCGCGTGATGGGCATCCTGAAGAACTACCAGCAGTGGTGGATGTGGGGCATCTGGGCTTCTGGATGCTGATCA
TCAGCAGCGTGGTGGGCAACCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCCT
GTTCTGCACCAGCGACGCCAAGGCCTACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCC
GACCCCAACCCCCAGGAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACC
AGATGCACGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGAC
CCTGAAGTGCCGCAACGTGAACGCCACCAACAACATCAACAGCATGATCGACAACAGCAACAAGGGCGAGATGAAG
AACTGCAGCTTCAACGTGACCACCGAGCTGCGCGACCGCAAGCAGGAGGTGCACGCCCTGTTCTACCGCCTGGACG
TGGTGCCCTGACAGGGCAACAACAGCAACGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCCAGGCCTG
CCCCAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGACCCCCGCGGCTACGCCATCCTGAAGTGCAACAAC
CAGACCTTCAACGGCACCGGCCCTGCAACAACGTGAGCAGCGTGAGTGCGCCACGGCATCAAGCCCGTGGTGA
GCACCCAGCTGCTGCTGAACGGCAGCCTGGCCAAGGGCGAGATCATCATCCGCAGCGAGAACCTGGCCAACAACGC
CAAGATCATCATCGTGAGCTGAACAAGCCGTGAAGATCGTGTGCGTGCGCCCCAACAACAACACCCGCAAGAGC
GTGCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGCGGAGATCATCGGCGACATCCGCCAGGCCTACTGCATCA
TCAACAAGACCGAGTGGAACAGCACCTGACAGGGCGTGAGCAAGAAGCTGGAGGAGCACTTCAGCAAGAAGGCCAT
CAAGTTCGAGCCCAGCAGCGGCGGCGACCTGGAGATCACCAACACAGCTTCAACTGCCGCGCGGAGTTCTTCTAC
TGCGACACCAGCCAGCTGTTCAACAGCACCTACAGCCCCAGCTTCAACGGCACCGAGAACAAGCTGAACGGCACCA
TCACCATCACTGCCGCATCAAGCAGATCATCAACATGTGGCAGAAGTGGGCCGCGCCATGTACGCCCCCCCCAT
CGCCGGCAACCTGACCTGCGAGAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGACCGGCCCAAC
GACACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACGGCGCAACGAGCTGTACAAGTACAAGGTGG
TGGAGATCAAGCCCTGGGCGTGCCCCCACCAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGTGGG
CATCGGCGCCGTGTTCTGGGCTTCTGGGCGCCGCCGCGCAGCACCATGGGCGCCGCCAGCATCACCTGACCGTG
CAGGCCCCGCTGCTGCTGAGCGGCATCGTGACGAGCAGACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACC
TGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGACCCGATCCTGGCCGTGGAGCGCTACCTGAAGGACCA
GCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACAGCAGCTGGAGC
AACCGCAGCCACGACGAGATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAGATCAACAACCTACACCGACA
CCATCTACCGCCTGCTGGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGCCCTGGACAGCTG
GCAGAACCTGTGGAACCTGGTTTACGATCACCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGC
CTGATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGCCCT
TCCAGACCCTGACCCCAACCCCCGCGAGCCCGACCGCCTGGGCCGCGATCGAGGAGGAGGGCGGCGAGCAGGACCG
CGGCCGCGCATCCGCTGCTGAGCGGCTTCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTGTTTACG
TACCACCGCCTGCGCGACTTCATCTGATCGCCGCCCGCGTGTGGAGCTGCTGGGCCAGCGCGGCTGGGAGGCC
TGAAGTACCTGGGCAGCCTGGTGCACTACTGGGGCTGGAGCTGAAGAAGAGCGCCATCAGCCTGCTGGACACCAT
CGCCATCGCCGTGGCCGAGGGCACCGCATCATCGAGTTTATCCAGCGCATCTGCCGCGCCATCCGCAACATC
CCCCCGCGCATCCGCCAGGGCTTCGAGGCCGCCCTGCAGTAA

Fig. 4

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--> signal peptide (1-72) \-->
ATGCGCGTGC GCGGCATCCTGCGCAGCTGGCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATCTGCAGCG
gp120/140/160 (72)
GCCTGGGCAACCTGTGGGTGACCGTGTACGACGGCGTGCCCGTGTGGCGCGAGGCCAGCACCACCCTGTTCTGCGC
CAGCGACGCCAAGGCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCGACCCCAAC
CCCCAGGAGATCGAGCTGGACAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCAAG
AGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCCGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGAAGTG
CACCAACTACAGCACCAACTACAGCAACACCATGAACGCCACCAGCTACAACAACAACACCACCGAGGAGATCAAG
AACTGCACCTTCAACATGACCACCGAGCTGCGCGACAAGAAGCAGCAGGTGTACGCCCTGTTCTACAAGCTGGACA
TCGTGCCCTGAACAGCAACAGCAGCGAGTACCGCTGATCAACTGCAACACCAGCGCCATCACCAGGCCTGCC
CAAGGTGAGCTTCGACCCCATCCCATCCACTACTGCGCCCCGCGGCTACGCCATCCTGAAGTGCAAGAACAAC
ACCAGCAACGGCACCGGCCCTGCCAGAACGTGAGCACCCTGCACTGCAACCCACGGCATCAAGCCCGTGGTGAGCA
CCCCCTGCTGCTGAACGGCAGCCTGGCCGAGGGCGGCGAGATCATCATCCGAGCAAGAACCTGAGCAACAACGC
CTACACCATCATCGTGCACCTGAACGACAGCGTGGAGATCGTGTGACCCGCCCAACAACAACACCCGCAAGGGC
ATCCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGAGAATCATCGGCGACATCCGCCAGGCCCACTGCAACA
TCAGCGCCGGCGAGTGGAAACAAGCCGTGAGCGCGTGAAGCTGCGCGAGCACTTCCCCAACAAGACCAT
CGAGTTCAGCCCAGCAGCGGGCGGACCTGGAGATCACCAACCACAGCTTCAACTGCCCGGGCGAGTTCTTCTAC
TGCAACACCAGCAAGCTGTTCAACAGCAGCTACAACGGCACCAGCTACCGCGGCACCGAGAGCAACAGCAGCATCA
TCACCCTGCCCTGCCGCATCAAGCAGATCATCGACATGTGGCAGAAGGTGGGCCGCGCCATCTACGCCCCCCCCAT
CGAGGGCAACATCACCTGCAGCAGCAGCATACCGGCCTGCTGCTGGCCCGGACGGCGGCCTGGACAACATCACC
ACCGAGATCTTCCGCCCCAGGGCGGCGACATGAAGGACAACCTGGCGCAACGAGCTGTACAAGTACAAGTTGGTGG
AGATCAAGCCCTGGGCGTGGCCCCCACCAGGCCAAGCGCCGCTGGTGGAGCGCGAGAAGCGCGCCGTGGGCAT
CGGGCGCGTGATCTTCGGCTTCTGGGCGCCCGGCGAGCAACATGGGCGCCCGCAGCATCACCTGACCGCCCAG
GCCCCGAGCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAACCTGCTGCGCGCCATCGAGGCCAGCAGCACATGC
TGCAGCTGACCGTGTGGGCATCAAGCAGCTGCAGGCCCGCTGCTGGCCATCGAGCGCTACCTGAAGGACCAGCA
GCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAAC
AAGACCCAGGGCGAGATCTGGGAGAACATGACCTGGATGCAGTGGGACAAGGAGATCAGCAACTACACCGGCATCA
TCTACCGCCTGCTGGAGGAGAGCCAGAACCAGCAGGAGCAGAACGAGAAGGACCTGCTGGCCCTGGACAGCCGCAA
CAACCTGTGGAGCTGGTTCAACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGCGGCCTG
ATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCTGCGCCAGGGCTACAGCCCCCTGAGCTTCC
AGACCCTGACCCCCAACCCCGCGGCTGGACCGCTGGGCCGATCGAGGAGGAGGGCGGCGAGCAGGACCGCGA
CCGAGCATCCGCTGGTGCAGGGCTTCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTGTTAGCTAC
CACCGCCTGCGCGACCTGATCCTGGTGACCGCCCGCTGGTGGAGCTGCTGGGCCGAGCAGCCCCCGCGCCTGC
AGCGCGGTGGGAGGCCCTGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCTGGAGCTGAAGAAGAGCGCCAC
CAGCCTGCTGGACAGCATCGCCATCGCCGTGGCCGAGGGCACCGCATCATCGAGGTGATCCAGCGCATCTAC
CGCGCCTTCTGCAACATCCCCCGCGCGTGGCCAGGGCTTCGAGGCCGCTGCAGTAA
gp120 (1509) <-- \--> (1510) gp41
gp140 (2022) <-- \/
gp160, gp41 (2565) <-- \

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ATGGGGGCGCCGCGCCAGCATCCTGCGCGGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCCTGCGCCCCGG
CGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGAAGTTCGCCCTGAACC
CCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATCCGCCAGCTGCACCCCGCCCTGCAGACCGGC
AGCGAGGAGCTGAAGAGCCTGTTCAACACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTGCG
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGARGATCCAGCAGGCCG
AGGCCGCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCAC
CAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGT
GATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACCATGCGTGAACACCGTGG
GCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCCGCGAGTGGGAACCGGTG
CACCCCGTGACGCGCGGCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCAC
CACCAGCACCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTACA
AGCGCTGGATCATCCTGGGCCTGAACAAGATCGTGCCATGTACAGCCCCGTGAGCATCCTGGACATCAAG
CAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGAGCAC
CCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCC
TGCGCGCCCTGGCCCCGGCGCCAGCCTGGAGGAGATGATGACCGCTGCCAGGGCGTGGGCGGCCCCAGC
CACAAAGGCCCGCGTCTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCG
CCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGGCCAG
GCCAACTTCTGGGCAAGATCTGGCCAGCCACAAGGGCGCCCCCGGCAACTTCTGCGAGAGCCGCCCCGA
GCCACCGCCCCCCCCCGCGAGAGCTTCGCTTCGAGGAGACCACCCCGGCCAGAAGCAGGAGAGCAAGG
ACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCCGCAACGACCCCTGAGCCAGTAA

Figure 5

Gag_AF110967_BW_opt

ATGGGGCGCCCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCCTGCGCCCGG
CGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGGGGCTTCCCCCTGAACC
CCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGC
ACCGAGGAGCTGCGCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCACGCCCGCATCGAGGTCCG
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGAGCCAGCAGAAGACCCAGCAGGCCA
AGGAGGCCGACGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAG
GCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGAT
CCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACACCGTGGGCG
GCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCAC
CCCGTGCAGGCCGGCCCCCGTGGCCCCCGGCCAGATGCGCGACCCCGCGGCAGCGACATCGCCGGCGCCAC
CAGCAOCCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCGTGCCCGTGGGCGACATCTACAAGC
CGTGGATCATCCTGGGCCTGAACAAGATCGTGCCTATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAG
GGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCCTGCGCGCCGAGCAGGCCACCCA
GGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGC
GCGCCTGGGGCCCGCGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCGGCCAC
AAGGCCCGCGTGTGGCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAAGTGGCGG
CCCCCGCAAGAAGGGCTGCTGGAAGTGCAGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG
GCCAACTTCTGGGCAAGATCTGGCCAGCCACAAGGGCCCGCCCGGCAACTTCTGCAGAACCGCAGCGA
GCCCCCGCCCCACCGTGCCACCGCCCCCCCCCGCGAGAGCTTCCGCTTCGAGGAGACCACCCCGCCC
CCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCTGACCGCCCTGCGCAGCCTGTTCCGGCAGC
GGCCCCCTGAGCCAGTAA

Figure 6

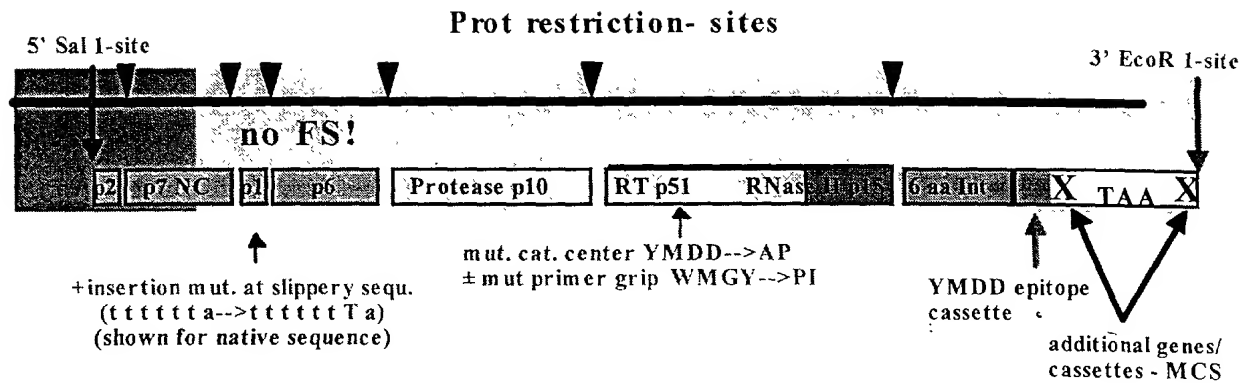


FIGURE 7

PR975(+) (SEQ ID NO:30)

GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGAT
GCAGCGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAA
GGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGT
GCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTC
CGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAA
CCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCA
GCGAGGCCGCGCCGAGCGCCAGGGCACCTGAACTTCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGTGGAC
ACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCC
CAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT
GATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCGT
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCAT
CAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGG
TGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG
GAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACAC
CCCCGTGTTCCGCATCAAGAAGAAGGACAGCACCAAGTGCGCAAGCTGGTGGA
TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCC
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCC
TACTTCAGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTACCATCCCC
AGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGC
TGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTC
CGCGCCCGCAACCCCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGG
AGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCT
GCTGCGCTGGGGCTTACCACCCCGACAAGAAGCACCAAGAGAGCCCCCTTCTCT
GTGGATGGGCTACGAGCTGCACCCCGACAAGTGGAACCGTGACGCCATCGAGCTGCC
CGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACT
GGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCG
GCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTG
GCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGACGGCGTGTACTACGACCCAG
CAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGAACCTACCAGA
TCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACC
GCCCACACCAACGACGTGAAGCAGCTGACCGAGGCGGTGCAGAAGATCGCCATGGA
GAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCATCCAGAAGGAGAC
CTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTT
CGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCAT
CGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCAGCGAGACCAAGATCGGCA
AGGCCGGCTACGTGACCGACCGGGGCCGCGCAGAAGATCGTGAGCCTGACCGAGACC
ACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAG
CGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCC
CGACAAGAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGG
AGAAGGTGTACCTGAGCTGGGTGCCCGCCACAAGGGCATCGGCGGCAACGAGCAG
ATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCTTGGACGGCATCGAT
GGCGGCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCGAGCGGCGGCCCT
AGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGTGAATTC

FIGURE 8

PR975YM (SEQ ID NO:31)

GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGAT
GCAGCGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAA
GGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGGTGCTGGAAGT
GCGGCAAGGAGGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTC
CGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAA
CCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCA
GCGAGGCCGGCGCCGAGCGCCAGGGCACCTGAACCTTCCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGAC
ACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCC-
CAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT
GATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCGT
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACCTTCCCCAT
CAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGG
TGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG
GAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCGGAGAACCCCTACAACAC
CCCCGTGTTTCGCCATCAAGAAGAAGGACAGCACCAAGTGCGCGCAAGCTGGTGGACT
TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCC
TACTTCAGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCC
AGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGC
TGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTC
CGCGCCCGCAACCCCGAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGAC
CTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCG
CTGGGGCTTACCAACCCCGACAAGAAGCACCAAGGAGCCCCCTTCTGTGGAT
GGGCTACGAGCTGCACCCCGACAAGTGACCGTGACGCCATCGAGCTGCCCGAGA
AGGAGAGCTGGACCGTGAAACGACATCCAGAAGCTGGTGGGCAAGCTGAACCTGGGCC
AGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCC
AAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGA
GAACCGCGAGATCCTGCGCGAGCCCGTGACGCGCGTGTACTACGACCCAGCAAGG
ACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTAC
CAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCA
CACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCA
TCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGG
AGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGA
ACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG
CCGAGACCTTCTACGTGGACGGCGCCGCAACCGCGAGACCAAGATCGGCAAGGCC
GGCTACGTGACCGACCGGGGCGGCAGAAAGATCGTGAGCCTGACCGAGACCACCAA
CCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGG
TGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCGACA
AGAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAG
GTGTACCTGAGCTGGGTGCCCGCCACAAGGGCATCGGCGGCAACGAGCAGATCGA
CAAGCTGGTGAAGGGCATCCGCAAGGTGCTGTTCTGGACGGCATCGATGGCG
GCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGA
TCGATTAAGGCTTCCCGGGGCTAGCACCGGTGAATTC

FIGURE 9

PR975YMWM (SEQ ID NO:32)

GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGAT
GCAGCGCAGCAACTTCAAGGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAA
GGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGT
GCGGCAAGGAGGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTC
CGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAA
CCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCA
GCGAGGCCGGCGCCGAGCGCCAGGGCACCTGAACTTCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGAC
ACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCC
CAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT
GATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCCGT
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCAT
CAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGG
TGAAGCAGTGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG
GAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACAC
CCCCGTGTTCCGATCAAGAAGAAGGACAGCACCAAGTGCGCAAGCTGGTGGACT
TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCC
TACTTCAGCGTGCCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCC
AGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGC
TGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTC
CGCGCCCCGCAACCCCCGAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGAC
CTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCG
CTGGGGCTTCACCACCCCCGACAAGAAGCACCAAGGAGCCCCCTTCCTGCCCAT
CGAGCTGCACCCCCGACAAGTGGAACCGTGACGCCATCGAGCTGCCCCGAGAAGGAGA
GCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAG
ATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCC
CTGACCGACATCGTGCCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCG
CGAGATCCTGCGCGAGCCCCGTGCACGGCGTGTACTACGACCCAGCAAGGACCTGGT
GGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGC
CCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCCACCAAC
GACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGAT
CTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCT
GGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCC
CCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAG
ACCTTCTACGTGGACGGCGCCGCAACCGCGAGACCAAGATCGGCAAGGCCGGCTA
CGTGACCGACCGGGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAACCAGA
AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAAC
ATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCCGACAAGAG
CGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGT
ACCTGAGCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAG
CTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCTTGACGGCATCGATGGCGGCATC
GTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGAT
TAAAGCTTCCCGGGGCTAGCACCGGTGAATTC

FIGURE 10

8_5_ZA (SEQ ID NO:33)

1 TGGAAGGGTT AATTTACTCC AAGAAAAGGC AAGAAATCCT TGATTTGTGG GTCTATCACA
61 CACAAGGCTT CTTCCCTGAT TGGCAAACT ACACACCGGG GCCAGGGGTC AGATATCCAC
121 TGACCTTTGG ATGGTGCTAC AAGCTAGTGC CAGTTGACCC AGGGGAGGTG GAAGAGGCCA
181 ACGGAGGAGA AGACAACGTG TTGCTACACC CTATGAGCCA ACATGGAGCA GAGGATGAAG
241 ATAGAGAAGT ATTAAAGTGG AAGTTTGACA GCCTCCTAGC ACGCAGACAC ATGGCCCGCG
301 AGCTACATCC GGAGTATTAC AAAGACTGCT GACACAGAAG GGACTTTCCG CCTGGGACTT
361 TCCACTGGGG CGTTCCGGGA GGTGTGGTCT GGGCGGGACT TGGGAGTGGT CAACCTCAG
421 ATGCTGCATA TAAGCAGCTG CTTTTCGCCCT GTACTGGGTC TCTCTCGGTA GACCAGATCT
481 GAGCCTGGGA GCCCTCTGGC TATCTAGGGA ACCCACTGCT TAAGCCTCAA TAAAGCTTGC
541 CTTGAGTGCT TTAAGTAGTG TGTGCCCATC TGTTGTGTGA CTCTGGTAAC TAGAGATCCC
601 TCAGACCCTT TGTGGTAGTG TGGAAAATCT CTAGCAGTGG CGCCCGAACA GGGACCAGAA
661 AGTGAAAGTG AGACCAGAGG AGATCTCTCG ACGCAGGACT CGGCTTGCTG AAGTGCACAC
721 GGCAAGAGGC GAGAGGGGCG GCTGGTGAGT ACGCCAATTT TACTTGACTA GCGGAGGCTA
781 GAAGGAGAGA GATGGGTGCG AGAGCGTCAA TATTAAGCGG CGGAAAATTA GATAAATGGG
841 AAAGAATTAG GTTAAGGCCA GGGGGAAGA AACATTATAT GTTAAACAT CTAGTATGGG
901 CAAGCAGGGA GCTGGAAAGA TTTGCACTTA ACCCTGGCCT GTTAGAAACA TCAGAAGGCT
961 GTAAACAAAT AATAAACAG CTACAACCAG CTCTTCAGAC AGGAACAGAG GAACCTTAGAT
1021 CATTATTCAA CACAGTAGCA ACTCTCTATT GTGTACATAA AGGGATAGAG GTACGAGACA
1081 CCAAGGAAGC CTTAGACAAG ATAGAGGAAG AACAAAACAA ATGTCAGCAA AAAGCACAAAC
1141 AGGCAAAAGC AGCTGACGAA AAGGTCAGTC AAAATTATCC TATAGTACAG AATGCCCAAG
1201 GGCAAAATGGT ACACCAAGCT ATATCACCTA GAACATTGAA TGCATGGATA AAAGTAATAG
1261 AGGAAAAGGC TTTCAATCCA GAGGAAATAC CCATGTTTAC AGCATTATCA GAAGGAGCCA
1321 CCCCACAAGA TTAAACACA ATGTTAAATA CAGTGGGGGG ACATCAAGCA GCCATGCAAA
1381 TGTTAAAAGA TACCATCAAT GAGGAGGCTG CAGAATGGGA TAGGACACAT CCAGTACATG
1441 CAGGGCCTGT TGCACCAGGC CAGATGAGAG AACCAAGGGG AAGTGACATA GCAGGAACTA
1501 CTAGTACCCT TCAGGAACAA ATAGCATGGA TGACAAGTAA TCCACCTATT CCAGTAGAAG
1561 ACATCTATAA AAGATGGATA ATTCTGGGGT TAAATAAAAT AGTAAGAATG TATAGCCCTG
1621 TTAGCATTTT GGACATAAAA CAAGGGCCAA AAGAACCCTT TAGAGACTAT GTAGACCGGT
1681 TCTTTAAAC CTTAAGAGCT GAACAAGCTA CACAAGATGT AAAGAATTGG ATGACAGACA
1741 CTTGTTGGT CCAAATGCG AACCAGATT GTAAGACCAT TTTAAGAGCA TTAGGACCAG
1801 GGGCCTCATT AGAAGAAATG ATGACAGCAT GTCAGGGAGT GGGAGGACCT AGCCATAAG
1861 CAAGAGTGTT GGCTGAGGCA ATGAGCCAAG CAAACAGTAA CATACTAGTG CAGAGAAGCA
1921 ATTTTAAAGG CTCTAACAGA ATTATTAAAT GTTCAACTG TGGCAAAGTA GGGCACATAG
1981 CCAGAAATTG CAGGGCCCCT AGGAAAAGG GCTGTTGGAA ATGTGGACAG GAAGGACACC
2041 AAATGAAAGA CTGTACTGAG AGGCAGGCTA ATTTTTTAGG GAAAATTTGG CCTTCCCACA
2101 AGGGGAGGCC AGGGAATTTT CTCCAGAACA GACCAGAGCC AACAGCCCCA CCAGCAGAAC
2161 CAACAGCCCC ACCAGCAGAG AGCTTCAGGT TCGAGGAGAC AACCCCGTG CCGAGGAAGG
2221 AGAAAGAGAG GGAACCTTTA ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTTGTCTC
2281 AATAAAAGTA GAGGGCCAGA TAAAGGAGGC TCTCTTAGAC ACAGGAGCAG ATGATACAGT
2341 ATTAGAAGAA ATAGATTTGC CAGGGAATG GAAACCAAAA ATGATAGGGG GAATTGGAGG
2401 TTTTATCAAA GTAAGACAGT ATGATCAAAT ACTTATAGAA ATTTGTGGAA AAAAGGCTAT
2461 AGGTACAGTA TTAGTAGGGC CTACACCAGT CAACATAATT GGAAGAAATC TGTTAACTCA
2521 GCTTGATGTC AACTAAATT TTCCAATTAG TCCTATTGAA ACTGTACCAG TAAATTTAAA
2581 ACCAGGAATG GATGGCCCAA AGGTCAAACA ATGGCCATTG ACAGAAGAAA AAATAAAAGC
2641 ATTAACAGCA ATTTGTGAGG AAATGGAGAA GGAAGGAAAA ATTACAAAAA TTGGGCGCTGA
2701 TAATCCATAT AACACTCCAG TATTTGCCAT AAAAAAGAA GACAGTACTA AGTGGAGAAA
2761 ATTAGTAGAT TTCAGGGAAC TCAATAAAG AACTCAAGAC TTTTGGGAAG TTCAATTAGG
2821 AATACCACAC CCAGCAGGAT TAAAAAGAA AAAATCAGTG ACAGTGCTAG ATGTGGGGGA
2881 TGCATATTTT TCAGTTCCTT TAGATGAAAG CTTCAGGAAA TATACTGCAT TCACCATACC

FIGURE 11

2941 TAGTATAAAC AATGAAACAC CAGGGATTAG ATATCAATAT AATGTGCTGC CACAGGGATG
3001 GAAAGGATCA CCAGCAATAT TCCAGAGTAG CATGACAAAA ATCTTAGAGC CCTTCAGAGC
3061 AAAAAATCCA GACATAGTTA TCTATCAATA TATGGATGAC TTGTATGTAG GATCTGACTT
3121 AGAAATAGGG CAACATAGAG CAAAAATAGA AGAGTTAAGG GAACATTTAT TGAAATGGGG
3181 ATTTACAACA CCAGACAAGA AACATCAAAA AGAACCCCA TTTCTTTGGA TGGGGTATGA
3241 ACTCCATCCT GACAAATGGA CAGTACAACC TATACTGCTG CCAGAAAAGG ATAGTTGGAC
3301 TGTCAATGAT ATACAGAAGT TAGTGGGAAA ATTAACTGG GCAAGTCAGA TTTACCCAGG
3361 GATTAAAGTA AGGCAACTCT GTAACTCCT CAGGGGGGCC AAAGCACTAA CAGACATAGT
3421 ACCACTAACT GAAGAAGCAG AATTAGAATT GGCAGAGAAC AGGGAAATTT TAAGAGAACC
3481 AGTACATGGA GTATATTATG ATCCATCAAA AGACTTGATA GCTGAAATAC AGAAACAGGG
3541 GCATGAACAA TGGACATATC AAATTTATCA AGAACCATTT AAAATCTGA AAACAGGGAA
3601 GTATGCAAAA ATGAGGACTA CCCACACTAA TGATGTAAAA CAGTTAACAG AGGCAGTGCA
3661 AAAAAATAGCC ATGGAAAGCA TAGTAATATG GGGAAAGACT CCTAAATTTA GACTACCCAT
3721 CCAAAAAGAA ACATGGGAGA CATGGTGGAC AGACTATTGG CAAGCCACCT GGATCCCTGA
3781 GTGGGAGTTT GTTAATACCC CTCCCCTAGT AAAATTATGG TACCAACTAG AAAAAGATCC
3841 CATAGCAGGA GTAGAACTT TCTATGTAGA TGGAGCAACT AATAGGGGAG CTAAATAGG
3901 AAAAGCAGGG TATGTTACTG ACAGAGGAAG GCAGAAAATT GTTACTCTAA CTAACACAAC
3961 AAATCAGAAG ACTGAGTTAC AAGCAATTCA GCTAGCTCTG CAGGATTTCAG GATCAGAAGT
4021 AAACATAGTA ACAGACTCAC AGTATGCATT AGGAATCATT CAAGCACAAC CAGATAAGAG
4081 TGACTCAGAG ATATTTAACC AAATAATAGA ACAGTTAATA AACAAGGAAA GAATCTACCT
4141 GTCATGGGTA CCAGCACATA AAGGAATTGG GGGAAATGAA CAAGTAGATA AATTAGTAAG
4201 TAAGGGAATT AGGAAAGTGT TGTCTCTAGA TGGAAATAGAT AAAGCTCAAG AAGAGCATGA
4261 AAGGTACCAC AGCAATTGGA GAGCAATGGC TAATGAGTTT AATCTGCCAC CCATAGTAGC
4321 AAAAGAAAATA GTAGCTAGCT GTGATAAATG TCAGCTAAAA GGGGAAGCCA TACATGGACA
4381 AGTCGACTGT AGTCCAGGGA TATGGCAATT AGATTGTACC CATTTAGAGG GAAAAATCAT
4441 CCTGGTAGCA GTCCATGTAG CTAGTGGCTA CATGGAAGCA GAGGTTATCC CAGCAGAAAC
4501 AGGACAAGAA ACAGCATATT TTATATTTAA ATTAGCAGGA AGATGGCCAG TCAAAGTAAT
4561 ACATACAGAC AATGGCAGTA ATTTTACCAG TACTGCAGTT AAGGCAGCCT GTTGGTGGGC
4621 AGGTATCCAA CAGGAATTTG GAATTCCTTA CAATCCCCAA AGTCAGGGAG TGGTAGAATC
4681 CATGAATAAA GAATTAAAGA AAATAATAGG ACAAGTAAGA GATCAAGCTG AGCACCTTAA
4741 GACAGCAGTA CAAATGGCAG TATTCATTCA CAATTTTAAA AGAAAAGGGG GAATTGGGGG
4801 GTACAGTGCA GGGGAAAGAA TAATAGACAT AATAGCAACA GACATACAAA CTAAAGAATT
4861 ACAAAAACAA ATTATAAGAA TTCAAAATTT TCGGGTTTAT TACAGAGACA GCAGAGACCC
4921 TATTTGGAAA GGACCAGCCG AACTACTCTG GAAAGGTGAA GGGGTAGTAG TAATAGAAGA
4981 TAAAGGTGAC ATAAAGGTAG TACCAAGGAG GAAAGCAAAA ATCATTAGAG ATTATGGAAA
5041 ACAGATGGCA GGTGCTGATT GTGTGGCAGG TGGACAGGAT GAAGATTAGA GCATGGAATA
5101 GTTTAGTAAA GCACCATATG TATATATCAA GGAGAGCTAG TGGATGGGTC TACAGACATC
5161 ATTTTGAAAG CAGACATCCA AAAGTAAGTT CAGAAGTACA TATCCCATTA GGGGATGCTA
5221 GATTAGTAAT AAAACATAT TGGGGTTTGC AGACAGGAGA AAGAGATTGG CATTTGGGTC
5281 ATGGAGTCTC CATAGAATGG AGACTGAGAG AATACAGCAC ACAAGTAGAC CCTGACCTGG
5341 CAGACCAGCT AATTCACATG CATTATTTTG ATTGTTTTAC AGAATCTGCC ATAAAGACAAG
5401 CCATATTAGG ACACATAGTT TTTCTAGGT GTGACTATCA AGCAGGACAT AAGAAGGTAG
5461 GATCTCTGCA ATACTTGGCA CTGACAGCAT TGATAAAACC AAAAAAGAGA AAGCCACCTC
5521 TGCCTAGTGT TAGAAAATTA GTAGAGGATA GATGGAACGA CCCCAGAAG ACCAGGGGCC
5581 GCAGAGGGAA CCATACAATG AATGGACACT AGAGATTCTA GAAGAACTCA AGCAGGAAGC
5641 TGTCAGACAC TTTCTAGAC CATGGCTCCA TAGCTTAGGA CAATATATCT ATGAAACCTA
5701 TGGGGATACT TGGACGGGAG TTGAAGCTAT AATAAGAGTA CTGCAACAAC TACTGTTTCAT
5761 TCATTTTCTA ATTGGATGCC AACATAGCAG AATAGGCATC TTGCGACAGA GAAGAGCAAG
5821 AAATGGAGCC AGTAGATCCT AAATAAAGC CCTGGAACCA TCCAGGAAGC CAACCTAAAA
5881 CAGCTTGTA TAATTGCTTT TGCAAACT GTAGCTATCA TTGTCTAGTT TGCTTTCTAGA

FIGURE 11

5941 CAAAAGGTTT AGGCATTTCC TATGGCAGGA AGAAGCGGAG ACAGCGACGA AGCGCTCCTC
6001 CAAGTGGTGA AGATCATCAA AATCCTCTAT CAAAGCAGTA AGTACACATA GTAGATGTAA
6061 TGGTAAGTTT AAGTTTATTT AAAGGAGTAG ATTATAGATT AGGAGTAGGA GCATTGATAG
6121 TAGCACTAAT CATAGCAATA ATAGTGTGGA CCATAGCATA TATAGAATAT AGGAAATTGG
6181 TAAGACAAAA GAAAATAGAC TGGTTAATTA AAAGAATTAG GGAAAGAGCA GAAGACAGTG
6241 GCAATGAGAG TGATGGGGAC ACAGAAGAAT TGTCAACAAT GGTGGATATG GGGCATCTTA
6301 GGCTTCTGGA TGCTAATGAT TTGTAACACG GAGGACTTGT GGGTCACAGT CTACTATGGG
6361 GTACCTGTGT GGAGAGAAGC AAAAAGTACT CTATTCTGTG CATCAGATGC TAAAGCATAT
6421 GAGACAGAAG TGCATAATGT CTGGGCTACA CATGCTTGTG TACCCACAGA CCCCACCCA
6481 CAAGAAATAG TTTTGGGAAA TGTAACAGAA AATTTTAATA TGTGGAAAAA TAACATGGCA
6541 GATCAGATGC ATGAGGATAT AATCAGTTTA TGGGATCAAA GCCTAAAGCC ATGTGTAAAG
6601 TTGACCCAC TCTGTGTCAC TTTAACTGT ACAGATACAA ATGTTACAGG TAATAGAACT
6661 GTTACAGGTA ATACAAATGA TACCAATATT GCAAATGCTA CATATAAGTA TGAAGAAATG
6721 AAAAATTGCT CTTTCAATGC AACCACAGAA TTAAGAGATA AGAAACATAA AGAGTATGCA
6781 CTCTTTTATA AACTTGATAT AGTACCACTT AATGAAAATA GTAACAACTT TACATATAGA
6841 TTAATAAATT GCAATACCTC AACCATAACA CAAGCCTGTC CAAAGGTCTC TTTTGACCCG
6901 ATTCTTATAC ATTACTGTGC TCCAGCTGAT TATGCGATTG TAAAGTGTA TAATAAGACA
6961 TTCAATGGGA CAGGACCATG TTATAATGTC AGCACAGTAC AATGTACACA TGGAATTAAAG
7021 CCAGTGGTAT CAACTCAACT ACTGTAAAT GGTAGTCTAG CAGAAGAAGG GATAATAATT
7081 AGATCTGAAA ATTTGACAGA GAATACCAA ACAATAATAG TACATCTTAA TGAATCTGTA
7141 GAGATTAATT GTACAAGGCC CAACAATAAT ACAAGGAAAA GTGTAAGGAT AGGACCAGGA
7201 CAAGCATTCT ATGCAACAAA TGACGTAATA GGAAACATAA GACAAGCACA TTGTAACATT
7261 AGTACAGATA GATGGAATAA AACTTTACAA CAGGTAATGA AAAAATTAGG AGAGCATTTT
7321 CCTAATAAAA CAATAAAATT TGAACCACAT GCAGGAGGGG ATCTAGAAAT TACAATGCAT
7381 AGCTTTAATT GTAGAGGAGA ATTTTCTAT TGCAATACAT CAAACCTGTT TAATAGTACA
7441 TACTACCTTA AGAATGGTAC ATACAAATAC AATGGTAATT CAAGCTTACC CATCACACTC
7501 CAATGCAAAA TAAACAAAT TGTACGCATG TGGCAAGGGG TAGGACAAGC AATGTATGCC
7561 CCTCCCATTG CAGGAAACAT AACATGTAGA TCAAACATCA CAGGAATACT ATTGACACGT
7621 GATGGGGGAT TTAACAACAC AAACAACGAC ACAGAGGAGA CATTAGACC TGGAGGAGGA
7681 GATATGAGGG ATAAGTGGAG AAGTGAATTA TATAAATATA AAGTGGTAGA AATTAAGCCA
7741 TTGGGAATAG CACCCACTAA GGCAAAAAGA AGAGTGGTGC AGAGAAAAAA AAGAGCAGTG
7801 GGAATAGGAG CTGTGTTCTT TGGGTTCTTG GGAGCAGCAG GAAGCACTAT GGGCGCAGCG
7861 TCAATAACGC TGACGGTACA GGCCAGACAA CTGTTGTCTG GTATAGTGCA ACAGCAAAGC
7921 AATTTGCTGA AGGCTATAGA GCGCAACAG CATATGTTGC AACTCACAGT CTGGGGCATT
7981 AAGCAGCTCC AGGCGAGAGT CCTGGCTATA GAAAGATACC TAAAGGATCA ACAGCTCCTA
8041 GGGATTTGGG GCTGCTCTGG AAGACTCATC TGCACCACTG CTGTGCCTTG GAACTCCAGT
8101 TGGAGTAATA AATCTGAAGC AGATATTTGG GATAACATGA CTTGGATGCA GTGGGATAGA
8161 GAAATTAATA ATTACACAGA AACAATATTC AGGTTGCTTG AAGACTCGCA AAACCAGCAG
8221 GAAAAGAATG AAAAAGATTT ATTAGAATTG GACAAGTGGA ATAATCTGTG GAATTGGTTT
8281 GACATATCAA ACTGGCTGTG GTATATAAAA ATATTCATAA TGATAGTAGG AGGCTTGATA
8341 GGTTTAAGAA TAATTTTGC TGTGCTCTCT ATAGTGAATA GAGTTAGGCA GGGATACTCA
8401 CCTTTGTCAT TTCAGACCCT TACCCCAAGC CCGAGGGGAC TCGACAGGCT CGGAGGAATC
8461 GAAGAAGAAG GTGGAGAGCA AGACAGAGAC AGATCCATAC GATTGGTGAG CGGATTCTTG
8521 TCGCTTGCCCT GGGACGATCT GCGGAGCCTG TGCCCTCTCA GCTACCACCG CTTGAGAGAC
8581 TTCATATTAA TTGCAGTGAG GGCAGTGGA CTTCTGGGAC ACAGCAGTCT CAGGGGACTA
8641 CAGAGGGGGT GGGAGATCCT TAAGTATCTG GGAAGTCTTG TGCAGTATTG GGGTCTAGAG
8701 CTAAAAAAGA GTGCTATTAG TCCGCTTGAT ACCATAGCAA TAGCAGTAGC TGAAGGAACA
8761 GATAGGATTA TAGAATTGGT ACAAAGAATT TGTAAGAGCTA TCCTCAACAT ACCTAGGAGA
8821 ATAAGACAGG GCTTTGAAGC AGCTTTGCTA TAAATGGGA GGCAAGTGGT CAAAACGCAG
8881 CATAGTTGGA TGGCCTGCAG TAAGAGAAAG AATGAGAAGA ACTGAGCCAG CAGCAGAGGG
8941 AGTAGGAGCA GCGTCTCAAG ACTTAGATAG ACATGGGGCA CTTACAAGCA GCAACACACC

FIGURE 11

SEQ ID NO:34

GCTGAGGCAATGAGCCAAGCAACCAGCGCAAACATACTGATGCAGAGAAGCAATTT
CAAAGGCCCTAAAAGAATTATTAAATGTTTCAACTGTGGCAAGGAAGGGCACATAG
CTAGAAATTGTAGGGCCCCTAGGAAAAAAGGCTGTTGGAAATGTGGAAAGGAAGGA
CACCAAATGAAAGACTGTACTGAGAGGCAGGCTAA

FIGURE 12

105020" 5256560

975Pol wt until 6aa Int: (SEQ ID NO:35)

TTTTTTAGGGAAGATTTGGCCTTCCCAACAAGGGAAGGCCAGGGAATTTTCCTTCAGAA
CAGAACAGAGCCAACAGCCCCACCAGCAGAGAGCTTCAAGTTCGAGGAGACAACCC
CCGCTCCGAAGCAGGAGCCGAAAGACAGGGAACCTTAATTTCCCTCAAATCACTCT
TTGGCAGCGACCCCTTGTCTCAATAAAAGTAGGGGGTCAAATAAAGGAGGCTCTCTT
AGACACAGGAGCTGATGATACAGTATTAGAAGAAATGAGTTTGCCAGGAAAATGGA
AACCAAAAATGATAGGAGGAATTGGAGGTTTTATCAAAGTAAGACAGTATGATCAA
ATACTTATAGAAATTTGTGGAAAAAAGGCTATAGGTACAGTATTAATAGGACCTACA
CCTGTCAACATAATTGGAAGGAATATGTTGACTCAGCTTGGATGCACACTAAATTTT
CCAATTAGTCCCATTGAACTGTGCCAGTAAAAATTAAAGCCAGGAATGGATGGCCCA
AAGGTTAAACAATGGCCATTGACAGAAGAGAAAAATAAAAGCATTAAACAGCAATTTG
TGAAGAAATGGAGAAAAGAGGAAAAATTACAAAAATTGGGCCTGAAAATCCATATA
ACACTCCAGTATTTGCCATAAAAAAGAAGGACAGTACTAAGTGGAGAAAAGTTAGTA
GATTTTCAGGGAACCTTAATAAAAGAACTCAAGACTTTTGGGAAGTTCAATTAGGAATA
CCACACCCAGCAGGGTTAAAAAAGAAAAAATCAGTGACAGTACTGGATGTGGGGGA
TGCATATTTTTTCAGTTCCTTTAGATGAGGACTTCAGGAAATATACTGCATTCACCATA
CCTAGTATAAAACAATGAAACACCAGGGATTAGATATCAATATAATGTGCTTCCACAG
GGATGGAAAGGATCACCATCAATATTCCAGAGTAGCATGACAAAAATCTTAGAGCC
CTTTAGAGCAAGAAATCCAGAAATAGTCATCTATCAATATATGGATGACTTGTATGT
AGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAAAATAGAGGAGTTAAGAAAAC
ATCTGTAAAGGTGGGGATTTACCACACCGGACAAGAAACATCAGAAAGAACCCCCA
TTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACAGTACAGCCTATAGAG
TTGCCAGAAAAGGAAAGCTGGACTGTCAATGATATACAGAAGTTAGTGGGAAAATT
AAATTGGGCCAGTCAGATTTACCCAGGAATTAAAGTAAGGCAACTTTGTAACTCCT
TAGGGGGGCCAAAGCACTAACAGATATAGTACCACTAACTGAAGAAGCAGAATTAG
AATTGGCAGAGAACAGGGAAATTCTAAGAGAACCAGTACATGGAGTATATTATGAC
CCATCAAAAGACTTGGTAGCTGAAATACAGAAACAGGGGCATGACCAATGGACATA
TCAAATTTACCAAGAACCATTCAAAAACCTGAAAACAGGGAAGTATGCAAAAATGA
GGACTGCCCACACTAATGATGTAAAAACAGTTAACAGAGGCAGTGCAAAAAATAGCT
ATGGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAA
AGAAACATGGGAGACATGGTGGACAGACTATTGGCAAGCCACCTGGATTCTGAGT
GGGAGTTTGTTAATACCCCTCCCTTAGTAAAATTATGGTACCAGCTAGAGAAAGAAC
CCATAATAGGAGCAGAACTTTCTATGTAGATGGAGCAGCTAATAGGGAAACTAAA
ATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAAATTGTTTCTCTAAC
AGAAACAACAAATCAGAAGACTGAATTACAAGCAATTCAGCTAGCTTTGCAAGATT
AGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAG
CACAACCAGATAAGAGTGAATCAGAGTTAGTCAACCAAATAATAGAACAATTAATA
AAAAAGGAAAAGGTCTACCTGTCATGGGTACCAGCACATAAAGGAATTGGAGGAAA
TGAACAAATAGATAAATTAGTAAGTAAGGGAATCAGGAAAGTGCTGTTTCTAGATG
GAATAGAT

FIGURE 13

SEQ ID NO:36

GGCGGCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCG
GC

FIGURE 14

FIGURE 14

SEQ ID NO: 37

GGIVTYQYMDDLTVGSGG

FIGURE 15

105040"3456860

TGGAAGGGTTAATTTACTCCAGGAAAAGGCAAGAGATCCTTGATTTATGGGTCTATC
ACACACAAGGCTACTTCCCTGATTGGCAAACTACACACCGGGACCAGGGGTCAGA
TATCCACTGACCTTTGGATGGTGCTTCAAGCTAGTGCCAGTTGACCCAAGGGAAGTA
GAAGAGGCCAACGGAGGAGAAGACAACCTGTTTGCTACACCCTATGAGCCAGTATGG
AATGGATGATGAACACAAAGAAGTGTTACAGTGGAAGTTTGACAGCAGCCTAGCAC
GCAGACACCTGGCCCGCGAGCTACATCCGGATTATTACAAAGACTGCTGAÇACAGA
AGGGACTTTCCGCCTGGGACTTTCCACTGGGGCGTTCCAGGGGGAGTGGTCTGGGCG
GGACTGGGAGTGGCCAGCCCTCAGATGCTGCATATAAGCAGCGGCTTTTCGCCTGTA
CTGGGTCTCTCTAGGTAGACCAGATCCGAGCCTGGGAGCTCTCTGTCTATCTGGGGA
ACCCACTGCTTAGGCCTCAATAAAGCTTGCCTTGAGTGCTCTAAGTAGTGTGTGCCC
ATCTGTTGTGTGACTCTGGTAACTCTGGTAACTAGAGATCCCTCAGACCCTTTGTGGT
AGTGTGGAATACTCTAGCAGTGGCGCCCCGAACAGGGACTTGAAAGCGAAAGTGAG
ACCAGAGAAGATCTCTCGACGCAGGACTCGGCTTGCTGAAGTGCACTCGGCAAGAG
GCGAGGGGGGCGACTGGTGAGTACGCCAAAATTTTTTTTACTAGCGGAGGCTAGA
AGGAGAGAGATGGGTGCGAGAGCGTCAATATTAAGAGGGGGGAAAATTAGACAAAT
GGGAAAAAATTAGGTTACGGCCAGGGGGGAGAAAACACTATATGCTAAAACACCTA
GTATGGGCAAGCAGAGAGCTGGAAAGATTTGCAGTTAACCCTGGCCTTTTAGAGAC
ATCAGACGGATGTAGAC AAATAATAAAACAGCTACAACCAGCTCTTCAGA
CAGGAACAGAGGAAATTAGATCATTATTTAACACAGTAGCAACTCTCTATTGTGTAC
ATAAAGGGATAGATGTACGAGACACCAAGGAAGCCTTAGACAAGATAGAGGAGGA
ACAAAACAAATGTCAGCAAAAAACACAGCAGGCGGAAGCGGCTGACAAAAAGGTC
AGTCAAAATTATCCTATAGTGCAGAACCTCCAAGGGCAAATGGTACACCAGGCCAT
ATCACCTAGAACCCTGAATGCATGGGTAAAAGTAATAGAGGAGAAGGCTTTTAGCC
CAGAGGTAATACCCATGTTTACAGCATTATCAGAAGGAGCCACCCACAAGATTTA
AACACCATGTAAATACAGTGGGGGGACATCAAGCAGCCATGCAAATGTAAAAG
ATACCATCAATGAGGAGGCTGCAGAATGGGATAGGTTACATCCAGTACATGCAGGG
CCTGTTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACTA
CTAGTACCCTTCAAGAACAATAGCATGGATGACAAGTAACCCACCTATCCCAGTA
GGGGACATCTATAAAAGGTGGATAATTCTGGGGTTAAATAAAATAGTAAGAATGTA
CAGCCCTGTCAGCATTTTAGACATAAAACAAGGACCAAAGGAACCCTTTAGAGACT
ATGTAGACCGGTTCTTCAAACTTTAAGAGCTGAACAATCTACACAAGAGGTAAAA
AATTGGATGACAGACACCTTGTTAGTCCAAAATGCGAACCAGATTGTAAGACCATT
TTAAGAGCATTAGGACCAGGGGCTTCATTAGAAGAAATGATGACAGCATGTCAGGG
AGTGGGAGGACCTAGCCACAAAGCAAGAGTTTTGGCTGAGGCAATGAGCCAAGCAA
ACAATACAAGTGTAATGATACAGAAAAGCAATTTTAAAGGCCCTAGAAGAGCTGTT
AAATGTTTCAACTGTGGCAGGGAAGGGCACATAGCCAGGAATTGCAGGGCCCCCTAG
GAAAAGGGGCTGTTGGAAATGTGGAAAGGAAGGACACCAAATGAAAGACTGTACT
GAGAGGCAGGCTAATTTTTTAGGGAAAATTTGGCCTTCCCACAAGGGGAGGCCAGG
GAATTTCCCTTCAGAGCAGACCAGAGCCAACAGCCCCACCACTAGAACCAACAGCCC
CACCAGCAGAGAGCTTCAAGTTCAAGGAGACTCCGAAGCAGGAGCCGAAAGACAG
GGAACCTTTAACTTCCCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAA

FIGURE 16

GTAGCGGGCCAAACAAAGGAGGCTCTTTTAGATACAGGAGCAGATGATACAGTACT
 AGAAGAAATAAACTTGCCAGGAAAATGGAAACCAAAAATGATAGGAGGAATTGGA
 GGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAGG
 GCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTG
 TTGACTCAGCTTGGATGCACACTAAATTTTCCAATTAGCCCCATTGAACTGTACCA
 GTAAAATTAAGCCAGGAATGGATGGCCCAAAGGTAAACAATGGCCATTGACAGA
 AGAAAAAATAAAAGCATTAAACAGAAATTTGTGAGGAAATGGAGAAGGAAGGAAAA
 ATTACAAAAATTGGGCCTGAAAATCCATATAACACTCCAGTATTTGCCATAAAGAAG
 AAGGACAGTACAAAGTGGAGAAAATTAGTAGATTTTCAGGGAACTCAATAAAAGAAC
 TCAAGACTTTTGGGAAGTCCAATTAGGAATACCACACCCAGCAGGGTTAAAAAAGA
 AAAAATCAGTGACAGTACTGGATGTGGGAGATGCATATTTTTCAGTCCCTTTAGATG
 AGAGCTTCAGAAAATATACTGCATTACCATACCTAGTATAAACAATGAAACACCA
 GGGATTAGATATCAATATAATGTTCTTCCACAGGGATGGAAAGGATCACCAGCAA
 TATTCCAGAGTAGCATGACAAGAATCTTAGAGCCCTTTAGAACACAAAACCCAGAA
 GTAGTTATCTATCAATATATGGATGACTTATATGTAGGATCTGACTTAGAAATAGGG
 CAACATAGAGCAAAAATAGAGGAGTTAAGAGGACACCTATTGAAATGGGGATTTAC
 CACACCAGACAAGAAACATCAGAAAGAACCCCCATTTCTTTGGATGGGGTATGAAC
 TCCATCCTGACAAATGGACAGTACAGCCTATACAGCTGCCAGAAAAGGAGAGCTGG
 ACTGTCAATGATATACAGAAAGTTAGTGGGAAAGTTAACTGGGCAAGTCAGATTTA
 CCCAGGGATTAAAGTAAGGCAACTGTGTAAACTCCTTAGGGGAGCCAAAGCACTAA
 CAGACATAGTGCCACTGACTGAAGAAGCAGAATTAGAATTGGCTGAGAACAGGGA
 AATTCTAAAAGAACAGTACATGGAGTATATTATGACCCATCAAAAAGATTTAATAG
 CTGAAATACAGAAACAGGGGAATGACCAATGGACATATCAAATTTACCAAGAACC
 ATTTAAAAATCTGAGAACAGGAAAGTATGCAAAAATGAGGACTGCCCACACTAATG
 ATGTGAAACAGTTAGCAGAGGCAGTGCAAAAGATAACCCAGGAAAGCATAGTAATA
 TGGGGAAAAACTCCTAAATTTAGACTACCCATCCCAAAAAGAAACATGGGAGACATG
 GTGGTCAGACTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTGTCAATACCCC
 TCCCCTAGTAAAATTGTGGTACCAGCTGGAAAAAGAACCCATAGTAGGGGCAGAAA
 CTTTCTATGTAGATGGAGCAGCCAATAGGGAAACTAAAATAGGAAAAGCAGGGTAT
 GTCACTGACAAAGGAAGGCAGAAAGTTGTTTCCTTCACTGAAACAACAAATCAGAA
 GACTGAATTACAAGCAATTCAGCTAGCTTTGCAGGATTCAGGGCCAGAAGTAAACA
 TAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGT
 GAATCAGAATTAGTCAGTCAAATAATAGAACAGTTGATAAAAAAGGAAAAAGTCTA
 CCTATCATGGGTACCAGCACATAAAGGAATTGGAGGAAATGAACAAGTAGACAAAT
 TAGTAAGTAGTGGAATCAGAAAAGTACTGTTTCTAGATGGAATAGATAAAGCTCAA
 GAAGAGCATGAAAAATATCACAGCAATTGGAGAGCAATGGCTAGTGAGTTTAATCT
 GCCACCCATAGTAGCAAAGGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAG
 GGAAGCCATGCATGGACAAGTCGACTGTAGTCCAGGAATATGGCAATTAGACTGT
 ACACATTTAGAAGGAAAAATCATCCTAGTAGCAGTCCATGTAGCCAGTGGCTACAT
 GGAAGCAGAGGTTATCCAGCAGAAACAGGACAAGAAACAGCATACTTTATACTAA
 AATTAGCAGGAAGATGGCCAGTCAAAGTAATACATACAGATAATGGCAGTAATTC
 ACCAGTACCGCAGTTAAGGCAGCCTGTTGGTGGGCAGATATCCAACGGGAATTTGG
 AATCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCCATGAATAAAGAATTAA

FIGURE 16

AGAAAATCATAGGGCAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAA
ATGGCAGTATTCATTACAAATTTTAAAAAGAAAAGGGGGGATTGGGGGGTACAGTGC
AGGGGAGAGAATAATAGACATAATAGCATCAGACATACAACTAAAGAATTACAAA
AACAAATTATAAAAATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCCTA
TTTGGAAGAGGACCAGCCAACTACTCTGGAAAGGTGAAGGGGCAGTAGTAATACAA
GATAATAGTGATATAAAGGTAGTACCAAGAAGGAAAAGCAAAAATCATTAAAGGACTA
TGGAACACAGATGGCAGGTGCTGATTGTGTGGCAGGTAGACAGGATGAAGATTAGA
ACATGGCACAGTTTAGTAAAGCACCATATGTATGTTTCGAGGAGAGCTGATGGATGG
TTCTACAGACATCATTATGAAAGCAGACACCCAAAAGTAAGTTCAGAAGTACACAT
CCCATTAGGAGATGCCAGGTAGTAATAAAAACATATTGGGGTCTGCAGACAGGAG
AAAGAGCTTGGCATTGGGGTCACGGAGTCTCCATAGAATGGAGATTGAGAAGATAT
AGCACACAAGTAGACCCTGACCTGACAGACCACTAATTCATATGCATTATTTTGAT
TGTTTTGCAGAATCTGCCATAAGGAAAGCCATACTAGGACAGATAGTTAGCCCTAA
GTGTGACTATCAAGCAGGACATAACAAGGTAGGATCTCTACAATACTTGGCACTGA
CAGCATTGATAAAACCAAAAAAGATAAAGCCACCTCTGCCTAGTGTTAGGAAATTA
GTAGAGGATAGATGGAACAAGCCCCAGAAGACCAGGGGCCGAGAGGGAACCATA
CAATGAATGGACACTAGAGCTTTTAGAAGAACTCAAGCAGGAAGCTGTCAGACACT
TTCCTAGACCATGGCTCCATACTTAGGACAACATATCTATGAAACCTATGGAGATA
CTTGACAGGAGTTGAAGCAATAATAAGAATCCTGCAACAATTACTGTTTATTATT
TCAGGATTGGGTGCCATCATAGCAGAATAGGCATTTTGCAGACAGAGAAGAGCAAGA
AATGGAGCCAATAGATCCTAACCTAGAACCCTGGAACCATCCAGGAAGTCAGCCTA
AACTGCTTGTAATGGGTGTTACTGTAAACGTTGCAGCTATCATTGTCTAGTTTGCTT
TCAGAAAAAAGGCTTAGGCATTTACTATGGCAGGAAGAAGCGGAGACAGCGACGAA
GCGCTCCTCCAAGCAATAAAGATCATCAAGATCCTCTACCAAAGCAGTAAGTACCG
AATAGTATATGTAATGTTAGATTAACTGCAAGAATAGATTCTAGATTAGGAATAGG
AGCATTGATAGTAGCACTAATCATAGCAATAATAGTGTGGACCATAGTATATATAG
AATATAGGAAATTGGTAAGGCAAAGGAAAATAGACTGGTTAGTTAAAAGGATTAGG
GAAAGAGCAGAAGACAGTGGCAATGAGAGCGAGGGGGATACTGAAGAATTATCGA
CACTGGTGGATATGGGGCATCTTAGGCTTTTGGATGCTAATGATGTGTAATGTGAA
GGGCTTGTGGGTCACAGTCTACTACGGGGTACCTGTGGGGAGAGAAGCAAAAAT
ACTCTATTTTGTGCATCAGATGCTAAAGCATATGAGAAAGAAGTGCATAATGTCTG
GGCTACACATGCCTGTGTACCCACAGACCCCAACCCACAAGAAGTGATTTTGGGC
AATGTAACAGAAAAATTTTAACATGTGGAATAATGACATGGTGGATCAGATGCAGG
AAGATATAATCAGTTTATGGGATCAAAGCCTTAAGCCATGTGTAAAATTGACCCCA
CTCTGTGTCACTTTAACTGTACAAATGCAACTGTAACTACAATAATACCTCTAAA
GACATGAAAAATTGCTCTTTCTATGTAACCACAGAATTAAGAGATAAGAAAAAGAA
AGAAAATGCACTTTTTTATAGACTTGATATAGTACCACTTAATAATAGGAAGAATGG
GAATATTAACAACCTATAGATTAATAAATTGTAATACCTCAGCCATAACACAAGCCTG
TCCAAAAGTCTCGTTTGACCCAATTCTATACATTATTGTGCTCCAGCTGGTTATGCG
CCTCTAAAATGTAATAATAAGAAATTCAATGGAATAGGACCATGCGATAATGTCAG
CACAGTACAATGTACACATGGAATTAAGCCAGTGGTATCAACTCAATTACTGTTAAA
TGGTAGCCTAGCAGAAGAAGAGATAATAATTAGATCTGAAAATCTGACAAACAATG
TCAAAACAATAATAGTACATCTTAATGAATCTATAGAGATTAATGTACAAGACC

FIGURE 16

TGGCAATAATACAAGAAAGAGTGTGAGAATAGGACCAGGACAAGCATTCTATGCA
ACAGGAGACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAAAAATGA
ATGGAATACAACCTTTACAAAGGGTAAGTCAAAAATTACAAGAACTCTTCCCTAATA
GTACAGGGGATAAAATTTGCACCACACTCAGGAGGGGACCTAGAAATTACTACACAT
AGCTTTAATTGTGGAGGAGAATTTTTCTATTGCAATACAACAGACCTGTTTAATAGT
ACATACAGTAATGGTACATGCACTAATGGTACATGCATGTCTAATAATACAGAGCG
CATCACACTCCAATGCAGAATAAAACAAATTATAAACATGTGGCAGGAGGTAGGAC
GAGCAATGTATGCCCCCTCCATTGCAGGAAACATAACATGTAGATCAAATATTACA
GGACTACTATTAACACGTGATGGAGGAGATAATAACTGAAACAGAGACATTTCAG
ACCTGGAGGAGGAGACATGAGGGACAATTGGAGAAGTGAATTATATAAATACAAG
GTGGTAGAAATTAACCATTAGGAGTAGCACCCACTGCTGCAAAAAGGAGAGTGGT
GGAGAGAGAAAAAAGAGCAGTAGGAATAGGAGCTGTGTTCTTGGGTCTTGGGAG
CAGCAGGAAGCACTATGGGCGCAGCATCAATAACGCTGACGGTACAGGCCAGACAA
TTATTGTCTGGTATAGTGCAACAGCAAAGTAATTTGCTGAGGGCTATAGAGGCGCAA
CAGCATATGTTGCAACTCACGGTCTGGGGCATTAAAGCAGCTCCAGGCAAGAGTCCTG
GCTATAGAGAGATACCTACAGGATCAACAGCTCCTAGGACTGTGGGGCTGCTCTGG
AAAACCTCATCTGCACCCTAATGTGCTTTGGAACCTCTAGTTGGAGTAATAAACTCA
AAGTGATATTTGGGATAACATGACCTGGATGCAGTGGGATAGGGAAATTAGTAATT
ACACAAACACAATATACAGGTTGCTTGAAGACTCGCAAAGCCAGCAGGAAAGAAA
TGAAAAAGATTTACTAGCATTGGACAGGTGGAACAATCTGTGGAATTGGTTTAGCAT
AACAAATTGGCTGTGGTATATAAAAATATTCATAATGATAGTAGGAGGCTTGATAG
GTTTAAGAATAATTTTTGCTGTGCTCTCTCTAGTAAATAGAGTTAGGCAGGGATACT
CACCCTTGTCATTGCAGACCCTTATCCCAAACCCGAGGGGACCCGACAGGCTCGGA
GGAATCGAAGAAGAAGGTGGAGAGCAAGACAGCAGCAGATCCATTTCGATTAGTGA
GCGGATTCTTGACACTTGCTTGGGACGACCTACGAAGCCTGTGCCTCTTCTGCTACC
ACCGATTGAGAGACTTCATATTAATTGTAGTGAGAGCAGTGGAACCTTCTGGGACAC
AGTAGTCTCAGGGGACTGCAGAGGGGGTGGGGAACCTTAAGTATTTGGGGAGTCT
TGTGCAATATTGGGGTCTAGAGTTAAAAAAGAGTGCTATTAATCTGCTTGATACTAT
AGCAATAGCAGTAGCTGAAGGAACAGATAGGATTCTAGAATTCATACAAAACCTTT
GTAGAGGTATCCGCAACGTACCTAGAAGAATAAGACAGGGCTTCGAAGCAGCTTTG
CAATAAAATGGGGGGCAAGTGGTCAAAAAGCAGTATAATTGGATGGCCTGAAGTAA
GAGAAAGAATCAGACGAACCTAGGTCAGCAGCAGAGGGAGTAGGATCAGCGTCTCA
AGACTTAGAGAAACATGGGGCACTTACAACCAGCAACACAGCCCACAACAATGCTG
CTTGCGCCTGGCTGGAAGCGCAAGAGGAGGAAGGAGAAGTAGGCTTTCCAGTCAGA
CCTCAGGTACCTTTAAGACCAATGACTTATAAAGCAGCAATAGATCTCAGCTTCTTT
TTAAAAGAAAAGGGGGGACTGGAAGGGTTAATTTACTCCAAGAAAAGGCAAGAGAT
CCTTGATTTGTGGGTTTATAACACACAAGGCTTCTTCCCTGATTGGCAAACTACAC
ACCGGGACCAGGGGTCAGATTTCCACTGACCTTTGGATGGTACTTCAAGCTAGAGCC
AGTCGATCCAAGGGAAGTAGAAGAGGCCAATGAAGGAGAAAACAACCTGTTTACTAC
ACCCTATGAGCCAGCATGGAATGGAGGATGAAGACAGAGAAGTATTAAGATGGAAG
TTTGACAGTACGCTAGCACGCAGACACATGGCCCGCGAGCTACATCCGGAGTATTAC
AAAGACTGCTGACACAGAAGGGACTTTCCGCTGGGACTTTCCACTGGGGCGTTCCAG
GAGGTGTGGTCTGGGCGGGACAGGGGAGTGGTCAGCCCTGAGATGCTGCATATAAG
CAGCTGCTTTTCGCCTGTACTGGGTCTCTCTAGGTAGACCAGATCTGAGCCCGGGAG

FIGURE 16

[illegible]

1

>C4_Env_TV1_C_ZA_opt_short (SEQ ID NO:46)

CATCACCTGCAGTGCAAGATCAAGCAGATCGTGCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCCCATCG
CCGGCAACATCACCTGC

FIGURE 17

FIGURE 17

105040" 1236660

>C4_Env_TV1_C_ZA_opt (SEQ ID NO:47)

CTGCCCATCACCTGCAGTGCAAGATCAAGCAGATCGTGCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCC
CATCGCCGGCAACATCACCTGCCGCAGCAACATCACCGGCATCCTGCTGACCCGCGACGGCGGC

FIGURE 18

>C4_Env_TV1_C_ZA_wt (SEQ ID NO:48)

TTACCCATCACACTCCAATGCAAAATAAAACAAATTGTACGCATGTGGCAAGGGGTAGGACAAGCAATGTATGCCCCCTCC
CATTGCAGGAAACATAACATGTAGATCAAACATCACAGGAATACTATTGACACGTGATGGGGGA

FIGURE 19

FIGURE 19

>Envgp160_TV1_C_ZAopt (SEQ ID NO:49)

ATGCGCGTGATGGGCACCCAGAAGAACTGCCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATGCTGATGATCTG
CAACACCGAGGACCTGTGGGTGACCGTGACTACGGCGTGCCCGTGTTGGCGGAGGCCAAGACCACCCTGTTCTGCGCCA
GCGACGCCAAGGCCTACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCTGCGTGCCACCGACCCCCAACCCCGAG
GAGATCGTGCTGGGCAACGTGACCGAGAACTTCAACATGTGGAAGAACAACATGGCCGACCAGATGCACGAGGACATCAT
CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGACCTGAACTGCACCGACACCAACG
TGACCGGCAACCGCACCGTGACCGGCAACACCAACGACACCAACATCGCCAACGCCACCTACAAGTACGAGGAGATGAAG
AACTGCAGCTTCAACGCCACCCAGAGCTGCGCGACAAGAAGCACAAGGAGTACGCCCTGTTCTACAAGCTGGACATCGT
GCCCCGTAACGAGAACAGCAACAACCTTACCTACCGCCTGATCAACTGCAACACCAGCACCATCACCCAGGCCTGCCCCA
AGGTGAGCTTCGACCCCATCCCCATCCACTACTGCGCCCCCGCGACTACGCCATCCTGAAGTGCAACAACAAGACCTTC
AACGGCACCGGCCCCCTGCTACAACGTGAGCACCCTGCGTGCACCCACGGCATCAAGCCCGTGGTGAGCAACCCAGCTGCT
GCTGAACGGCAGCCTGGCCGAGGAGGGCATCATCATCCGCAGCGAGAACCCTGACCGAGAAACACCAAGACCATCATCGTGC
ACCTGAACGAGAGCGTGAGATCAACTGCACCCGCCCCAACACAACACCCGCAAGAGCGTGCGCATCGGCCCCGGCCAG
GCCTTCTACGCCACCAACGACGTGATCGGCAACATCCGCCAGGCCCACTGCAACATCAGCACCGACCGCTGGAACAAGAC
CCTGCGAGCAGGTGATGAAGAAGCTGGGCGAGCACTTCCCCAACAAAGACCATCAAGTTCGAGCCCCACGCCGGCGCGGACC
TGGAGATCACCATGCACAGCTTCAACTGCCGCGGCGAGTTCTTCTACTGCAACACCAGCAACCTGTTCAACAGCACCTAC
TACCCCAAGAACGGCACCTACAAGTACAACGGCAACAGCAGCCTGCCCATCACCTGCGAGTGAAGATCAAGCAGATCGT
GCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCCCATCGCCGGCAACATCACCTGCCGAGCAACATCACCG
GCATCCTGCTGACCCGCGACGGCGGCTTCAACAACACCAACAACGACACCGAGGAGACCTTCCGCCCCGGCGGCGGCGAC
ATGCGCGACAACCTGGCGCAGCGAGCTGTACAAGTACAAGTGTTGGAGATCAAGCCCTGGGCATCGCCCCACCAAGGC
CAAGCGCCGCGTGGTGACGCGAAGAAGCGCGCCGTGGGCATCGGCGCCGTGTTCTGGGCTTCTGGGCGCCGCGGCA
GCACCATGGGCGCCGCCAGCATCACCTGACCGTGACGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAAC
CTGCTGAAGGCCATCGAGGCCCTGAGGCCCAGCAGCATGCTGCGAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCGCTGCT
GGCCATCGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCCCGCTGATCTGCACCACCGCCG
TGCCCTGGAACAGCAGCTGGAGCAACAAGAGCGAGGCCGACATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAG
ATCAACAACCTACACCGAGACCATCTTCCGCCTGCTGGAGGACAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCT
GGAGCTGGACAAGTGGAAACAACCTGTGGAACCTGGTTGACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGA
TCGTGGGCGGCCGTGATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCC
CTGAGCTTCCAGACCCCTGACCCCCAGCCCCCGCGCCTGGACCGCCTGGGCGGCATCGAGGAGGAGGGCGGCGAGCAGGA
CCGCGACCGCAGCATCCGCCTGGTGAGCGGCTTCTGAGCCTGGCCTGGGACGACCTGCGCAGCCTGTGCCTGTTTCAGCT
ACCACCGCCTGCGCGACTTCATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAGCCTGCGCGGCCTGCAG
CGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGAGTACTGGGGCTGGAGCTGAAGAAGAGCGCCATCAGCCC
CCTGGACACCATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGCTGGTGAGCGCATCTGCCGCGCCATCC
TGAACATCCCCCGCCGATCCGCCAGGGCTTCGAGGCCGCCCTGCTGTAA

FIGURE 20

>Envgpl60_TV1_C_ZAwT (SEQ ID NO:50)

ATGAGAGTGATGGGGACACAGAAGAATTGTCAACAATGGTGGATATGGGGCATCTTAGGCTTCTGGATGCTAATGATTTG
TAACACGGAGGACTTGTGGGTACAGTCTACTATGGGGTACCTGTGTGGAGAGAAGCAAAACTACTCTATTCTGTGCAT
CAGATGCTAAAGCATATGAGACAGAAGTGCATAATGTCTGGGCTACACATGCTTGTGTACCCACAGACCCCAACCCACAA
GAAATAGTTTTGGGAAATGTAACAGAAAATTTTAATATGTGGAAAAATAACATGGCAGATCAGATGCATGAGGATATAAT
CAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAGTTGACCCCACTCTGTGTCACTTTAAACTGTACAGATACAAATG
TTACAGGTAATAGAACTGTTACAGGTAATACAAATGATACCAATATTGCAAATGCTACATATAAGTATGAAGAAATGAAA
AATTGCTCTTTCAATGCAACCACAGAATTAAGAGATAAGAAACATAAAGAGTATGCACTCTTTTATAAACTTGATATAGT
ACCACTTAATGAAAATAGTAACAACCTTTACATATAGATTAATAAATTGCAATACCTCAACCATAACACAAGCCTGTCCAA
AGGTCTCTTTTGACCCGATTCTTATACATTACTGTGCTCCAGCTGATTATGCGATTCTAAAGTGTAAATAAAGACATTC
AATGGGACAGGACCATGTTATAATGTCAGCACAGTACAATGTACACATGGAATTAAGCCAGTGGTATCAACTCAACTACT
GTTAAATGGTAGTCTAGCAGAAGAAGGGATAATAATTAGATCTGAAAATTTGACAGAGAATACCAAAACAATAATAGTAC
ATCTTAATGAATCTGTAGAGATTAATTGTACAAGGCCCAACAATAATACAAGGAAAAGTGTAAAGGATAGGACCAGGACAA
GCATTCTATGCAACAAATGACGTAATAGGAAACATAAGACAAGCACATTGTAACATTAGTACAGATAGATGGAATAAAAC
TTTACAACAGGTAATGAAAAAATTAGGAGAGCATTTCCCTAATAAAACAATAAAATTTGAACCACATGCAGGAGGGGATC
TAGAAATTACAATGCATAGCTTTAATTGTAGAGGAGAAATTTTCTATTGCAATACATCAAACCTGTTTAATAGTACATAC
TACCTTAAGAATGGTACATACAAATACAATGGTAATTCAAGCTTACCCATCACACTCCAATGCAAAATAAAACAAATTGT
ACGCATGTGGCAAGGGGTAGGACAAGCAATGTATGCCCTCCCATTCAGGAAACATAACATGTAGATCAAACATCACAG
GAATACTATTGACACGTGATGGGGGATTTAACAACACAAACAACGACACAGAGGAGACATTGAGACCTGGAGGAGGAGAT
ATGAGGGATAACTGGAGAAGTGAATTATATAAATATAAAGTGGTAGAAATTAAGCCATTGGGAATAGCACCCCACTAAGGC
AAAAAGAAGAGTGGTGCAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCTTGGGTCTTGGGAGCAGCAGGAA
GCACTATGGGCGCAGCGTCAATAACGCTGACGGTACAGGCCAGACAACCTGTTGTCTGGTATAGTGCAACAGCAAAGCAAT
TTGCTGAAGGCTATAGAGGCGCAACAGCATATGTTGCAACTCACAGTCTGGGGCATTAAGCAGCTCCAGGCGAGAGTCTT
GGCTATAGAAAAGATACCTAAAGGATCAACAGCTCCTAGGGATTTGGGGCTGCTCTGGAAGACTCATCTGCACCACTGCTG
TGCCTTGGAACCTCAGTTGGAGTAATAAATCTGAAGCAGATATTTGGGATAACATGACTTGGATGCAGTGGGATAGAGAA
ATTAATAATTACACAGAAACAATATTTCAGGTTGCTTGAAGACTCGCAAAACCAGCAGGAAAAGAATGAAAAAGATTTATT
AGAATTGGACAAGTGAATAATCTGTGGAATTGGTTTGACATATCAAACCTGGCTGTGGTATATAAAAAATATTCATAATGA
TAGTAGGAGGCTTGATAGGTTTAAGAATAATTTTTGCTGTGCTCTCTATAGTGAATAGAGTTAGGCAGGGATACTCACCT
TTGTCAATTCAGACCCCTTACCCCAAGCCCCGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGA
CAGAGACAGATCCATACGATTGGTGAGCGGATTCTTGTGCTTGCCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCT
ACCACCGCTTGAGAGACTTCATATTAATTGCAGTGAGGGCAGTGGAACCTTCTGGGACACAGCAGTCTCAGGGGACTACAG
AGGGGGTGGGAGATCCTTAAGTATCTGGGAAGTCTTGTGCAGTATTGGGGTCTAGAGCTAAAAAAGAGTGCCTATTAGTCC
GCTTGATACCATAGCAATAGCAGTAGCTGAAGGAACAGATAGGATTATAGAATTGGTACAAAGAATTTGTAGAGCTATCC
TCAACATACCTAGGAGAATAAGACAGGGCTTTGAAGCAGCTTTGCTATAA

FIGURE 21

>Gag_TV1_C_ZAopt (SEQ ID NO:51)

ATGGGCGCCCGCGCCAGCATCCTGAGCGGCGGCAAGCTGGACAAGTGGGAGCGCATCCGCCTGCGCCCCGGCGGCAAGAA
GCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGCGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCA
GCGAGGGCTGCAAGCAGATCATCAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTTCAAC
ACCGTGGCCACCCTGTACTGCGTGCACAAGGGCATCGAGGTGCGCGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGA
GCAGAACAAGTGCCAGCAGAAGGCCAGCAGGCCAAGGCCGCGACGAGAAGGTGAGCCAGAACTACCCCATCGTGCAGA
ACGCCCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCTGAACGCCTGGATCAAGGTGATCGAGGAGAAGGCC
TTCAACCCCGAGGAGATCCCCATGTTCAACGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACAC
CGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCGGAGTGGGACCGCACCCACC
CCGTGCACGCGCGCCCGTGGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCACCAGCACCCCTG
CAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGAGGACATCTACAAGCGCTGGATCATCCTGGGCCT
GAACAAGATCGTGCATGTACAGCCCCGTGAGCATCCTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACG
TGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGGCCACCCAGGACGTGAAGAACTGGATGACCGACACCCTGCTGGTG
CAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCCCTGGGCCCCGGCGCCAGCCTGGAGGAGATGATGACCGCCTG
CCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGTGGCCGAGGCCATGAGCCAGGCCAACAGCAACATCCTGGTGC
AGCGCAGCAACTTCAAGGGCAGCAACCGCATCATCAAGTGCTTCAACTGCGGCAAGGTGGGCCACATCGCCCGCAACTGC
CGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCCAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAA
CTTCCTGGGCAAGATCTGGCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAACCGCCCCGAGCCCCACCGCCCCC
CCGCCGAGCCCACCGCCCCCCCCGCGGAGAGCTTCCGCTTCGAGGAGACCACCCCGTGCCCCGCAAGGAGAAGGAGCGC
GAGCCCCTGACCAGCCTGAAGAGCCTGTTCCGCAGCGACCCCTGAGCCAGTAA

FIGURE 22

>Gag_TV1_ZA_MHROpt (SEQ ID NO:53)

GACATCAAGCAGGGCCCCAAGGAGCCCTTCGCGACTACGTGGACCGCTTCTTCAAGACC

FIGURE 24

FIGURE 24

>Gag_TV1_ZA_MHRwt (SEQ ID NO:54)

GACATAAAACAAGGGCCAAAAGAACCCTTTAGAGACTATGTAGACCGGTTCTTTAAAACC

FIGURE 25

FIGURE 25

>Nef_TV1_C_ZAopt (SEQ ID NO:55)

ATGGGCGGCAAGTGGAGCAAGCGCAGCATCGTGGGCTGGCCCGCCGTGCGCGAGCGCATGCGCCGCACCGAGCCCGCCGC
CGAGGGCGTGGGCGCCGCCAGCCAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCGCCACCAACGAGG
CCTGCGCCTGGCTGCAGGCCCAGGAGGAGGACGGCGACGTGGGCTTCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATG
ACCTACAAGAGCGCCGTGGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTACAGCCGCAAGCG
CCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCTTCTTCCCCGACTGGCAGAACTACACCAGCGGCCCCGGCG
TGCGCTTCCCCCTGACCTTCGGCTGGTGCTTCAAGCTGGTGCCCGTGGACCCCGCGAGGTGAAGGAGGCCAACGAGGGC
GAGGACAAGTGCCTGCTGCACCCCATGAGCCAGCACGGCGCCGAGGACGAGGACCGCGAGGTGCTGAAGTGAAGTTCTGA
CAGCCTGCTGGCCACCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACTGCTGA

FIGURE 26

FIGURE 26

>Nef_TV1_C_ZAwT (SEQ ID NO:56)

ATGGGAGGCAAGTGGTCAAAACGCAGCATAGTTGGATGGCCTGCAGTAAGAGAAAGAATGAGAAGAACTGAGCCAGCAGC
AGAGGGAGTAGGAGCAGCGTCTCAAGACTTAGATAGACATGGGGCACTTACAAGCAGCAACACACCTGCTACTAATGAAG
CTTGTGCCTGGCTGCAAGCACAAGAGGAGGACGGAGATGTAGGCTTTCCAGTCAGACCTCAGGTACCTTTAAGACCAATG
ACTTATAAGAGTGCAGTAGATCTCAGCTTCTTTTAAAAGAAAAGGGGGGACTGGAAGGGTTAATTTACTCTAGGAAAAG
GCAAGAAATCCTTGATTTGTGGGTCTATAACACACAAGGCTTCTTCCCTGATTGGCAAACTACACATCGGGGCCAGGGG
TCCGATTCCCACTGACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGACCCAAGGGAGGTGAAAGAGGCCAATGAAGGA
GAAGACAACCTGTTTGCTACACCCTATGAGCCAACATGGAGCAGAGGATGAAGATAGAGAAGTATTAAAGTGGAAGTTTGA
CAGCCTTCTAGCACACAGACACATGGCCCGCGAGCTACATCCGGAGTATTACAAAGACTGCTGA

FIGURE 27

FIGURE 27

>NefD125G_TV1_C_ZAopt (SEQ ID NO:57)

ATGGGCGGCAAGTGGAGCAAGCGCAGCATCGTGGGCTGGCCCGCCGTGCGCGAGCGCATGCGCCGCACCGAGCCCGCCGC
CGAGGGCGTGGGCGCCGCCAGCCAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCGCCACCAACGAGG
CCTGCGCCTGGCTGCAGGCCCAGGAGGAGGACGGCGACGTGGGCTTCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATG
ACCTACAAGAGCGCCGTGGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTACAGCCGCAAGCG
CCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCTTCTTCCCCGGCTGGCAGAACTACACCAGCGGCCCCGGCG
TGCGCTTCCCCCTGACCTTCGGCTGGTGCTTCAAGCTGGTGCCCGTGGACCCCCGCGAGGTGAAGGAGGCCAACGAGGGC
GAGGACAACCTGCCTGCTGCACCCCATGAGCCAGCACGGCGCCGAGGACGAGGACCGCGAGGTGCTGAAGTGGAAGTTCGA
CAGCCTGCTGGCCCAACGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACTGCTGA

FIGURE 28

FIGURE 28

>p15RNaseH_TV1_C_ZAopt (SEQ ID NO:58)

ACCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCGCGGCCCGCCAGAA
GATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCG
AGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCGACAAGAGCGACAGCGAGATCTTC
AACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCGCCACAAGGGCATCGGCGGCAA
CGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATC

FIGURE 29

FIGURE 29

>p15RNaseH_TV1_C_Zawt (SEQ ID NO:59)

ACTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAA
AATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAGCTAGCTCTGCAGGATTCAGGATCAG
AAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGACTCAGAGATATTT
AACCAAATAATAGAACAGTTAATAAAACAAGGAAAGAATCTACCTGTCATGGGTACCAGCACATAAAGGAATTGGGGGAAA
TGAACAAGTAGATAAATTAGTAAGTAAGGGAATT

FIGURE 30

FIGURE 30

>p31Int_TV1_C_Zaopt (SEQ ID NO:60)

CGCAAGGTGCTGTTCTGGACGGCATCGACAAGGCCAGGAGGAGCAGAGCGCTACACAGCAACTGGCGCGCCATGGC
CAACGAGTTCAACCTGCCCCCATCGTGGCCAAGGAGATCGTGGCCAGCTGCGACAAGTGCCAGCTGAAGGGCGAGGCCA
TCCACGGCCAGGTGGACTGCAGCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGATCATCCTGGTGGCC
GTGCACGTGGCCAGCGGTACATGGAGGCCGAGGTGATCCCCGCCGAGACCGGCCAGGAGACCGCCTACTTCATCCTGAA
GCTGGCCGGCCGCTGGCCCGTGAAGGTGATCCACACCGACAACGGCAGCAACTTCACCAGCACCGCCGTGAAGGCCGCT
GCTGGTGGGCCGGCATCCAGCAGGAGTTCGGCATCCCCTACAACCCCCAGAGCCAGGGCGTGGTGGAGAGCATGAACAAG
GAGCTGAAGAAGATCATCGGCCAGGTGCGCGACCAGGCCGAGCACCTGAAGACCGCCGTGCAGATGGCCGTGTTTCATCCA
CAACTTCAAGCGCAAGGGCGGCATCGGCGGCTACAGCGCCGGCGAGCGCATCATCGACATCATCGCCACCGACATCCAGA
CCAAGGAGCTGCAGAAGCAGATCATCCGCATCCAGAACTTCCGCGTGACTACCGCGACAGCCGCGACCCCATCTGGAAG
GGCCCCGCCGAGCTGCTGTGGAAGGGCGAGGGCGTGGTGGTGATCGAGGACAAGGGCGACATCAAGGTGGTGGCCCCGCC
CAAGGCCAAGATCATCCGCGACTACGGCAAGCAGATGGCCGGCGCCGACTGCGTGGCCGGCGGCCAGGACGAGGAC

FIGURE 31

FIGURE 31

>p31Int_TV1_C_ZAwt (SEQ ID NO:61)

AGGAAAGTGTTGTTTCTAGATGGAATAGATAAAGCTCAAGAAGAGCATGAAAGGTACCACAGCAATTGGAGAGCAATGGC
TAATGAGTTTAATCTGCCACCCATAGTAGCAAAAGAAATAGTAGCTAGCTGTGATAAATGTCAGCTAAAAGGGGAAGCCA
TACATGGACAAGTCGACTGTAGTCCAGGGATATGGCAATTAGATTGTACCCATTTAGAGGGAAAAATCATCCTGGTAGCA
GTCCATGTAGCTAGTGGCTACATGGAAGCAGAGGTTATCCAGCAGAAACAGGACAAGAAACAGCATATTTTATATTAAA
ATTAGCAGGAAGATGGCCAGTCAAAGTAATACATACAGACAATGGCAGTAATTTTACCAGTACTGCAGTTAAGGCAGCCT
GTTGGTGGGCAGGTATCCAACAGGAATTTGGAATTCCTTACAATCCCCAAAGTCAGGGAGTGGTAGAATCCATGAATAAA
GAATTAAAGAAAAATAATAGGACAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAAATGGCAGTATTCATTCA
CAATTTTAAAGAAAAAGGGGAATTGGGGGTACAGTGCAGGGGAAAGAATAATAGACATAATAGCAACAGACATACAAA
CTAAAGAATTACAAAAACAAATTATAAGAATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCCTATTTGGAAA
GGACCAGCCGAACACTACTCTGGAAAGGTGAAGGGGTAGTAGTAATAGAAGATAAAGGTGACATAAAGGTAGTACCAAGGAG
GAAAGCAAAAATCATTAGAGATTATGGAAAACAGATGGCAGGTGCTGATTGTGTGGCAGGTGGACAGGATGAAGAT

FIGURE 32

FIGURE 32

>Pol_TV1_C_ZAopt (SEQ ID NO:62)

TTCTTCCGCGAGAACCTGGCCTTCCCCCAGGGCGAGGCCCGCGAGTTCCCCCGAGCAGACCCGCGCCAACAGCCCCAC
CAGCCGCACCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCGCGCCGAGGAGGGCGAGCGCGAGG
GCACCTTCAACTTCCCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCC
CTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGG
CATCGGCGGCTTCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG
TGGTGGGCCCCACCCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCCTGAACCTTCCCCATCAGC
CCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAA
GATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCGGACAAACCCCTACA
ACACCCCGTGTTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGC
ACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCACCCCGCGGCCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGA
CGTGGGCGACGCTACTTACGCGTGCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTACCATCCCCAGCATCAACA
ACGAGACCCCGGCATCCGCTACCACTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGC
ATGACCAAGATCCTGGAGCCCTTCCGCGCCAAGAACCCGACATCGTGATCTACCAGTACATGGACGACCTGTACGTGGG
CAGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTACCACCC
CCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACCGTGCGAGCCC
ATCCTGCTGCCCCGAGAAGGACAGCTGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACCTGGGCCAGCCAGAT
CTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGCGGCCAAGGCCCTGACCGACATCGTGCCCCTGACCG
AGGAGGCCGAGCTGGAGCTGGCCGAGAACC GCGAGATCCTGCGCGAGCCCGTGACGGCGTGTACTACGACCCAGCAAG
GACCTGATCGCCGAGATCCAGAAGCAGGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAA
GACCGGCAAGTACGCCAAGATGCGCACCAACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA
TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCTGCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACC
GACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCTGTAACACCCCCCTGGTGAAGCTGTGGTACCAGCTGGA
GAAGGACCCCATCGCCGGCGTGGAGACCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCT
ACGTGACCGACCGCGGCCGCGCAGAAGATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAG
CTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCC
CGACAAGAGCGACAGCGAGATCTTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGC
CCGCCCACAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCTTCTGGAC
GGCATCGACAAGGCCCAGGAGGAGCACGAGCGCTACCACAGCAACTGGCGCGCCATGGCCAACGAGTTCAACCTGCCCC
CATCGTGGCCAAGGAGATCGTGGCCAGCTGCGACAAGTGCCAGCTGAAGGGCGAGGCCATCCACGGCCAGGTGGACTGCA
GCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGATCATCCTGGTGGCCGTGCACGTGGCCAGCGGCTAC
ATGGAGGCCGAGGTGATCCCCGCGAGACCGGCCAGGAGACCGCCTACTTCATCCTGAAGCTGGCCGGCCGCTGGCCCCGT
GAAGGTGATCCACACCGACAACGGCAGCAACTTACCAGCACCGCCGTGAAGGCCGCTGCTGGTGGCCGGCATCCAGC
AGGAGTTCGGCATCCCCTACAACCCCGAGGCCAGGGCGTGGTGGAGAGCATGAACAAGGAGCTGAAGAAGATCATCGGC
CAGGTGCGCGACACGAGGCCGAGCACCTGAAGACCGCCGTGCAGATGGCCGTGTTTCATCCACAACCTTCAAGCGCAAGGGCGG
CATCGGCGGCTACAGCGCCGGCGAGCGCATCATCGACATCATCGCCACCGACATCCAGACCAAGGAGCTGCAGAAGCAGA
TCATCCGCATCCAGAACCTTCCGCGTGTACTACCGCGACAGCCGCGACCCCATCTGGAAGGGCCCCGCGAGCTGCTGTGG
AAGGGCGAGGGCGTGGTGGTATCGAGGACAAGGGCGCATCAAGGTGGTGCCCCCGCGCAAGGCCAAGATCATCCGCGA
CTACGGCAAGCAGATGGCCGGCGCGGACTGCGTGCCGGCGGGCCAGGACGAGGAC

FIGURE 33

>Pol_TV1_C_ZAwT (SEQ ID NO:63)

TTTTTTAGGGAAAATTTGGCCTTCCCACAAGGGGAGGCCAGGGAATTTCTCCAGAACAGACCAGAGCCAACAGCCCCAC
CAGCAGAACCAACAGCCCCACCAGCAGAGAGCTTCAGGTTTCGAGGAGACAACCCCCGTGCCGAGGAAGGAGAAAGAGAGG
GAACCTTTTAACTTCCCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAAGTAGAGGGCCAGATAAAGGAGGCT
CTCTTAGACACAGGAGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAATGATAGGGGG
AATTGGAGGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAAATTTGTGGAAAAAAGGCTATAGGTACAGTAT
TAGTAGGGCCTACACCAGTCAACATAATTGGAAGAAATCTGTTAACTCAGCTTGGATGCACACTAAATTTTCCAATTAGT
CCTATTGAAACTGTACCAGTAAAATTAACCAGGAATGGATGGCCCAAAGGTCAAACAATGGCCATTGACAGAAGAAAA
AATAAAGCATTAAACAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGATAATCCATATA
ACACTCCAGTATTTGCCATAAAAAAGGAAGGACAGTACTAAGTGGAGAAAAATTAGTAGATTTTCAGGGAACTCAATAAAGA
ACTCAAGACTTTTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAGAAAAAGAAAAATCAGTGACAGTGCTAGA
TGTGGGGGATGCATATTTTTCAGTTCCTTTAGATGAAAGCTTCAGGAAATATACTGCATTACCATACCTAGTATAAACA
ATGAAACACCAGGGATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTCAGAGTAGC
ATGACAAAAATCTTAGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAATATATGGATGACTTGTATGTAGG
ATCTGACTTAGAAATAGGGCAACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGATTACAAAC
CAGACAAGAAACATCAAAAAGAACCCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACAGTACAACCT
ATACTGCTGCCAGAAAAGGATAGTTGGACTGTCAATGATATACAGAAAGTTAGTGGGAAAATTAACCTGGGCAAGTCAGAT
TTACCCAGGGATTAAAGTAAGGCAACTCTGTAAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTACCACTAACTG
AAGAAGCAGAATTAGAATTGGCAGAGAACAGGGGAAATTTTAAGAGAACCAGTACATGGAGTATATTATGATCCATCAAAA
GACTTGATAGCTGAAATACAGAAACAGGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTTAAAAATCTGAA
AACAGGGAAGTATGCAAAAATGAGGACTACCCACACTAATGATGTAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCA
TGGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACATGGTGGACA
GACTATTGGCAAGCCACCTGGATCCCTGAGTGGGAGTTTGTTAATACCCCTCCCTAGTAAAATTATGGTACCAACTAGA
AAAAGATCCCATAGCAGGAGTAGAAAACTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAATAGGAAAAGCAGGGT
ATGTTACTGACAGAGGAAGGCAGAAAATTTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAG
CTAGCTCTGCAGGATTACAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAGCACAAACC
AGATAAGAGTGACTCAGAGATATTTAACCATAATAGAACAGTTAATAAACAAAGGAAAGAATCTACCTGTCATGGGTAC
CAGCACATAAAGGAATTGGGGGAAATGAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTGTTTCTAGAT
GGAATAGATAAAGCTCAAGAAGAGCATGAAAGGTACCACAGCAATTGGAGAGCAATGGCTAATGAGTTTAACTGCCCACC
CATAGTAGCAAAAGAAATAGTAGCTAGCTGTGATAAATGTCAGCTAAAAGGGGAAGCCATACATGGACAAGTCGACTGTA
GTCCAGGGATATGGCAATTAGATTGTACCCATTTAGAGGGAAAAATCATCCTGGTAGCAGTCCATGTAGCTAGTGGCTAC
ATGGAAGCAGAGGTTATCCCAGCAGAAACAGGACAAGAAACAGCATATTTTATATTTAAATTTAGCAGGAAGATGGCCAGT
CAAAGTAATACATACAGACAATGGCAGTAATTTTACCAGTACTGCAGTTAAGGCAGCCTGTTGGTGGGCAGGTATCCAAC
AGGAATTTGGAATTCCTACAATCCCCAAAGTCAGGGAGTGGTAGAATCCATGAATAAAGAATTAAAGAAAAATAATAGGA
CAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAAATGGCAGTATTCATTCACAATTTTAAAGAAAAGGGGG
AATTGGGGGGTACAGTGCAGGGGAAAGAATAATAGACATAATAGCAACAGACATACAACTAAAGAATTACAAAAACAAA
TTATAAGAATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCCTATTTGGAAAGGACCAGCCGAACCTACTCTGG
AAAGGTGAAGGGGTAGTAGTAATAGAAGATAAAGGTGACATAAAGGTAGTACCAAGGAGGAAAGCAAAAATCATTAGAGA
TTATGGAAAACAGATGGCAGGTGCTGATTGTGTGCAGGTGGACAGGATGAAGAT

FIGURE 34

>Prot_TV1_C_ZAopt (SEQ ID NO:64)

CCCCAGATCACCCGTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGACACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCCGGCAAGTGGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCTGAACTTC

FIGURE 35

FIGURE 35

>Prot_TV1_C_ZAwT (SEQ ID NO:65)

CCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGACACAGG
AGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTA
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA
CCAGTCAACATAATTGGAAGAAATCTGTAACTCAGCTTGGATGCACACTAAATTTT

FIGURE 36

103040"5256960

>Protina_TV1_C_ZAopt (SEQ ID NO:66)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGCCACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCGGCAAGTGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCTGAACTTC

FIGURE 37

FIGURE 37

>Protina_TV1_C_ZAwt (SEQ ID NO:67)

CCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGCCACAGG
AGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAATGATAGGGGGAATTGGAGGTTTTA
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA
CCAGTCAACATAATTGGAAGAAATCTGTAACTCAGCTTGGATGCACACTAAATTTT

FIGURE 38

105020" 5256860

>ProtinaRTmut_TV1_C_ZAopt (SEQ ID NO:68)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGCCACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCCGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCCTGAACTTCCCCATCAGCCCCATCGAGACCGT
GCCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGA
CCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACAACCCCTACAACACCCCGTGTTT
GCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTG
GGAGGTGCAGCTGGGCATCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCT
ACTTCAGCGTGCCCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGC
ATCCGCTACCAAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGAČCAAGATCCT
GGAGCCCTTCCGCGCCAAGAACCCCGACATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCC
AGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTACCACCCCGACAAGAAGCACCAGAAG
GAGCCCCCTTCCCTGCCATCGAGCTGCACCCCGACAAGTGGACCGTGACGCCCATCTGCTGCCCCGAGAAGGACAGCTG
GACCGTGAAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGC
TGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAG
AACC GCGAGATCCTGCGCGAGCCCGTGACGGCGTGTA CTACGACCCAGCAAGGACCTGATCGCCGAGATCCAGAAGCA
GGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCCGGCAAGTACGCCAAGATGCGCA
CCACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAG
ACCCCAAGTTCCGCGCTGCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCC
CGAGTGGGAGTTCTGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGACCCCATCGCCGGCGTGGAGA
CCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCGCGGCCGCCAGAAG
ATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGA
GGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCGACAAGAGCGACAGCGAGATCTTCA
ACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAAC
GAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG

FIGURE 39

>ProtinaRTmut_TV1_C_ZAwT (SEQ ID NO:69)

CCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGCCACAGG
AGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAATGATAGGGGGAATTGGAGGTTTTA
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA
CCAGTCAACATAATTGGAAGAAATCTGTAACTCAGCTTGGATGCACACTAAATTTTCCAATTAGTCCTATTGAACTGT
ACCAGTAAAATTAAACCAGGAATGGATGGCCCAAAGGTCAAACAATGGCCATTGACAGAAGAAAAAATAAAGCATTAA
CAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGATAATCCATATAAACTCCAGTATTT
GCCATAAAAAAGAAGGACAGTACTAAGTGAGAAAAATTAGTAGATTTTCAGGGAACTCAATAAAAGAAGTCAAGACTTTTG
GGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAAGAAAAATCAGTGACAGTGCTAGATGTGGGGGATGCAT
ATTTTTTCAGTTCCTTTAGATGAAAGCTTCAGGAAATATACTGCATTACCCATACCTAGTATAAACAATGAAACACCAGGG
ATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTCAGAGTAGCATGAÇAAAAATCTT
AGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAAGCCCCGTTGTATGTAGGATCTGACTTAGAAATAGGGC
AACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGATTTACAACACCAGACAAGAAACATCAAAAA
GAACCCCCATTTCTTCCCATCGAATCCATCCTGACAAATGGACAGTACAACCTATACTGCTGCCAGAAAAGGATAGTTG
GACTGTCAATGATATACAGAAGTTAGTGGGAAAAATTAACTGGGCAAGTCAGATTTACCCAGGGATTAAAGTAAGGCAAC
TCTGTAAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTACCCTAAGTGAAGAAGCAGAATTAGAATTGGCAGAG
AACAGGGAAATTTTAAGAGAACCAGTACATGGAGTATATTATGATCCATCAAAAGACTTGATAGCTGAAATACAGAAACA
GGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTTAAAAATCTGAAAAACAGGGAAGTATGCAAAAAATGAGGA
CTACCCCACTAATGATGTAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCATGGAAAGCATAGTAATATGGGGAAAG
ACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACATGGTGGACAGACTATTGGCAAGCCACCTGGATCCC
TGAGTGGGAGTTTGTTAATACCCCTCCCCTAGTAAAATTATGGTACCAACTAGAAAAAGATCCCATAGCAGGAGTAGAAA
CTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAAATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAA
ATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAGCTAGCTCTGCAGGATTCAGGATCAGA
AGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGACTCAGAGATATTTA
ACCAAATAATAGAACAGTTAATAAACAAGGAAAGAATCTACCTGTCTGTTGGTACCAGCACATAAAGGAATTGGGGGAAAT
GAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTTG

FIGURE 40

FIGURE 40

>ProtwtRTwt_TV1_C_ZAopt (SEQ ID NO:70)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGACACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCTGAACTTCCCCATCAGCCCCATCGAGACCGT
GCCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGA
CCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACAACCCCTACAACACCCCCGTGTTT
GCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTG
GGAGGTGCAGCTGGGCATCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCT
ACTTCAGCGTGCCCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTACCATCCCCAGCATCAACAACGAGACCCCCGGC
ATCCGCTACCAAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGAACAAGATCCT
GGAGCCCTTCCGCGCCAAGAACCCCGACATCGTGATCTACCAAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGA
TCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTACCACCCCCGACAAGAAGCAC
CAGAAGGAGCCCCCTTCTGTGGATGGGTACGAGCTGCACCCCGACAAGTGGACCGTGACGCCATCTGTGCTGCCCCGA
GAAGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCA
AGGTGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTG
GAGCTGGCCGAGAACC GCGAGATCTGCGGAGCCCGTGACGGCGTGTACTACGACCCAGCAAGGACCTGATCGCCGA
GATCCAGAAGCAGGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACG
CCAAGATGCGCACCAACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGAGAAGATCGCCATGGAGAGCATCGTG
ATCTGGGGCAAGACCCCAAGTTCCGCTGCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGC
CACCTGGATCCCCGAGTGGGAGTTCTGTAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGACCCCATCG
CCGGCGTGGAGACCTTCTACGTGGACGGCGCCACCAACCGCAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCGC
GGCCGCCAGAAGATCGTGACCCTGACCAACACCACCAACCGAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGA
CAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCGACAAGAGCGACA
GCGAGATCTTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCCGCCACAAGGGC
ATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG

FIGURE 41

>RevExon1_TV1_C_ZAopt (SEQ ID NO:72)

ATGGCCGGCCGCAGCGGCGACAGCGACGAGGCCCTGCTGCAGGTGGTGAAGATCATCAAGATCCTGTACCAGAGC

FIGURE 43

FIGURE 43

>RevExon1_TV1_C_ZAw1 (SEQ ID NO:73)

ATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGCTCCTCCAAGTGGTGAAGATCATCAAAATCCTCTATCAAAGCA

FIGURE 44

FIGURE 44

>RevExon2_TV1_C_ZAopt-2 (SEQ ID NO:74)

CCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCCCGCCGAACCGCCGCCGCTGGCGCGCCCGCCAGCGCCAGATCCA
CACCATCGGCGAGCGCATCCTGGTGGCCTGCCTGGGCCGCAGCGCCGAGCCCGTGCCCTGCAGCTGCCCCCCTGGAGC
GCCTGCACATCAACTGCAGCGAGGGCAGCGGCACCAGCGGCACCCAGCAGAGCCAGGGCACCACCGAGGGCGTGGGCGAC
CCCTAA

FIGURE 45

FIGURE 45

>RevExon2_TV1_C_ZAwT (SEQ ID NO:75)

ACCCTTACCCCAAGCCCGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATC
CATACGATTGGTGAGCGGATTCTTGTGCTTGCCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCGCTTGA
GAGACTTCATATTAATTGCAGTGAGGGCAGTGGAACCTCTGGGACACAGCAGTCTCAGGGGACTACAGAGGGGGTGGGAG
ATCCTTAA

FIGURE 46

FIGURE 46

RT_TV1_C_ZAopt (SEQ ID NO:76)

CCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCA
AGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCG
AGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACAACCCCTACAACA
CCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTT
CCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC
CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTAC
TTCAGCGTGCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTCACCATCCCCAGCA
TCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAA
GGGCAGCCCCGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCC
AAGAACCCCGACATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACC
TGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGT
GGGGCTTCACCACCCCGACAAGAAGCACCAAGGAGCCCCCCTTCCTGTGGATGGG
CTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCCTGCTGCCCCGAGAAGGAC
AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAG
ATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCC
TGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCG
AGATCCTGCGCGAGCCCGTGACCGGCGTGTACTACGACCCAGCAAGGACCTGATCGC
CGAGATCCAGAAGCAGGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTT
CAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCAACCCACACCAACGACGT
GAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGG
CAAGACCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACC
GACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCTGG
TGAAGCTGTGGTACCAGCTGGAGAAGGACCCCATCGCCGGCGTGGAGACCTTCTACGT
GGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCG
CGGCCGCCAGAAGATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCA
GGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAG
CCAGTACGCCCTGGGCATCATCCAGGCCAGCCCGACAAGAGCGACAGCGAGATCTTC
AACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCG
CCCACAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCC
GCAAGGTGCTG

FIGURE 47

>RT_TV1_C_ZAwT (SEQ ID NO:77)

CCAATTAGTCCTATTGAAACTGTACCAGTAAAAATTAAAACCAGGAATGGATGGCCCAAAGGTCAAACAATGGCCATTGAC
AGAAGAAAAAATAAAAGCATTAAACAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGATA
ATCCATATAACACTCCAGTATTTGCCATAAAAAAGAAGGACAGTACTAAGTGGAGAAAATTAGTAGATTTTCAGGGAACTC
AATAAAAGAACTCAAGACTTTTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAAGAAAAATCAGTGAC
AGTGCTAGATGTGGGGGATGCATATTTTTCAGTTCCTTTAGATGAAAGCTTCAGGAAATATACTGCATTACCCATACCTA
GTATAACAATGAAACACCAGGGATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTC
CAGAGTAGCATGACAAAAATCTTAGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAATATATGGATGACTT
GTATGTAGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGAT
TTACAACACCAGACAAGAAACATCAAAAAAGAACCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACA
GTACAACCTATACTGCTGCCAGAAAAGGATAGTTGGACTGTCAATGATATACAGAAGTTAGTGGGAAAATTAAACTGGGC
AAGTCAGATTTACCCAGGGATTAAAGTAAGGCAACTCTGTAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTAC
CACTAACTGAAGAAGCAGAATTAGAATTGGCAGAGAACAGGGAAATTTTAAGAGAACCAGTACATGGAGTATATTATGAT
CCATCAAAAGACTTGATAGCTGAAATACAGAAACAGGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTAA
AAATCTGAAAACAGGGAAGTATGCAAAAAATGAGGACTACCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAA
AAATAGCCATGGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACA
TGGTGGACAGACTATTGGCAAGCCACCTGGATCCCTGAGTGGGAGTTTGTTAATACCCCTCCCCTAGTAAATTTATGGTA
CCAACTAGAAAAAGATCCCATAGCAGGAGTAGAACTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAAATAGGAA
AAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAAATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAA
GCAATTCAGCTAGCTCTGCAGGATTAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTC
AGCACAACCAGATAAGAGTGACTCAGAGATATTTAACCAATAATAGAACAGTTAATAAACAAGGAAAGAATCTACCTGT
CATGGGTACCAGCACATAAAGGAATTGGGGGAAATGAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTG

FIGURE 48

FIGURE 48

>RTmut_TV1_C_ZAopt (SEQ ID NO:78)

CCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGAC
CGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACA
ACCCCTACAACACCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTG
AACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCACCCCGCCGGCTGAAGAAGAAGAAGAGCGTGAC
CGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTCACCATCCCCA
GCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTC
CAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCAAGAACCCCGACATCGTGATCTACCAGGCCCCCTGTACGT
GGGCAGCGACCTGGGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTCACCA
CCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGCCCATCGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATC
CTGCTGCCCCGAGAAGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTA
CCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGG
AGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTAACGACCCCGAGCAAGGAC
CTGATCGCCGAGATCCAGAAGCAGGGCCACGAGCAGTGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGAC
CGGCAAGTACGCCAAGATGCGCACCAACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGG
AGAGCATCGTGATCTGGGCAAGACCCCCAAGTTCGCCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGAC
TACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAA
GGACCCCATCGCCGGCGTGGAGACCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACG
TGACCGACCGCGGCCCGCCAGAAGATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTG
GCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCCGA
CAAGAGCGACAGCGAGATCTTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCCG
CCCACAAGGGCATCGGCGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG

FIGURE 49

FIGURE 49

>RTmut_TV1_C_ZAwT (SEQ ID NO:79)

CCAATTAGTCCTATTGAACTGTACCAGTAAATTTAAACCAGGAATGGATGGCCCAAAGGTCAAACAATGGCCATTGAC
AGAAGAAAAAATAAAAGCATTAAACAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGATA
ATCCATATAACACTCCAGTATTTGCCATAAAAAAGAAGGACAGTACTAAGTGGAGAAAATTAGTAGATTTTCAGGGAACTC
AATAAAAGAACTCAAGACTTTTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAAGAAAAATCAGTGAC
AGTGCTAGATGTGGGGGATGCATATTTTCAGTTCTTTTAGATGAAAGCTTCAGGAAATATACTGCATTCACCATACCTA
GTATAACAATGAAACACCAGGGATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTC
CAGAGTAGCATGACAAAAATCTTAGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAAGCCCCGTTGTATGT
AGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGATTACAA
CACCAGACAAGAAACATCAAAAAGAACCCCCATTTCTTCCCATCGAACTCCATCCTGACAAATGGACAGTACAACCTATA
CTGCTGCCAGAAAAGGATAGTTGGACTGTCAATGATATACAGAAGTTAGTGGGAAAATTAACTGGGCAAGTCAGATTTA
CCCAGGGATTAAAGTAAGGCAACTCTGTAAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTACCACTAACTGAAG
AAGCAGAATTAGAATTGGCAGAGAACAGGGAAATTTTAAGAGAACCAGTACATGGAGTATATTATGATCCATCAAAAGAC
TTGATAGCTGAAATACAGAAACAGGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTTAAAAATCTGAAAAC
AGGGAAGTATGCAAAAATGAGGACTACCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCATGG
AAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACATGGTGGACAGAC
TATTGGCAAGCCACCTGGATCCCTGAGTGGGAGTTTGTTAATACCCCTCCCCTAGTAAAAATTATGGTACCAACTAGAAAA
AGATCCCATAGCAGGAGTAGAACTTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAAATAGGAAAAGCAGGGTATG
TTACTGACAGAGGAAGGCAGAAAATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAGCTA
GCTCTGCAGGATTGAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAGCACAACCAGA
TAAGAGTGACTCAGAGATATTTAACCATAATAGAACAGTTAATAACAAGGAAAGAATCTACCTGTCATGGGTACCAG
CACATAAAGGAATTGGGGGAAATGAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTTG

FIGURE 50

09995-07694

Table 1. Demographic characteristics of the study population	
Age (years)	50.0 ± 10.0
Gender	
Male	50.0%
Female	50.0%
Education	
High school	50.0%
University	50.0%
Occupation	
Physician	50.0%
Nurse	50.0%
Other	50.0%
Marital status	
Married	50.0%
Single	50.0%
Divorced	50.0%
Widowed	50.0%
Religion	
Muslim	50.0%
Christian	50.0%
Jewish	50.0%
Hindu	50.0%
Buddhist	50.0%
Sikh	50.0%
Other	50.0%
Smoking status	
Smoker	50.0%
Non-smoker	50.0%
Alcohol consumption	
Alcoholic	50.0%
Non-alcoholic	50.0%
Family size	
1-2	50.0%
3-4	50.0%
5-6	50.0%
7-8	50.0%
9-10	50.0%
11-12	50.0%
13-14	50.0%
15-16	50.0%
17-18	50.0%
19-20	50.0%
21-22	50.0%
23-24	50.0%
25-26	50.0%
27-28	50.0%
29-30	50.0%
31-32	50.0%
33-34	50.0%
35-36	50.0%
37-38	50.0%
39-40	50.0%
41-42	50.0%
43-44	50.0%
45-46	50.0%
47-48	50.0%
49-50	50.0%
51-52	50.0%
53-54	50.0%
55-56	50.0%
57-58	50.0%
59-60	50.0%
61-62	50.0%
63-64	50.0%
65-66	50.0%
67-68	50.0%
69-70	50.0%
71-72	50.0%
73-74	50.0%
75-76	50.0%
77-78	50.0%
79-80	50.0%
81-82	50.0%
83-84	50.0%
85-86	50.0%
87-88	50.0%
89-90	50.0%
91-92	50.0%
93-94	50.0%
95-96	50.0%
97-98	50.0%
99-100	50.0%
101-102	50.0%
103-104	50.0%
105-106	50.0%
107-108	50.0%
109-110	50.0%
111-112	50.0%
113-114	50.0%
115-116	50.0%
117-118	50.0%
119-120	50.0%
121-122	50.0%
123-124	50.0%
125-126	50.0%
127-128	50.0%
129-130	50.0%
131-132	50.0%
133-134	50.0%
135-136	50.0%
137-138	50.0%
139-140	50.0%
141-142	50.0%
143-144	50.0%
145-146	50.0%
147-148	50.0%
149-150	50.0%
151-152	50.0%
153-154	50.0%
155-156	50.0%
157-158	50.0%
159-160	50.0%
161-162	50.0%
163-164	50.0%
165-166	50.0%
167-168	50.0%
169-170	50.0%
171-172	50.0%
173-174	50.0%
175-176	50.0%
177-178	50.0%
179-180	50.0%
181-182	50.0%
183-184	50.0%
185-186	50.0%
187-188	50.0%
189-190	50.0%
191-192	50.0%
193-194	50.0%
195-196	50.0%
197-198	50.0%
199-200	50.0%
201-202	50.0%
203-204	50.0%
205-206	50.0%
207-208	50.0%
209-210	50.0%
211-212	50.0%
213-214	50.0%
215-216	50.0%
217-218	50.0%
219-220	50.0%
221-222	50.0%
223-224	50.0%
225-226	50.0%
227-228	50.0%
2	

FIGURE 51

>TatExon1_TV1_C_ZAopt (SEQ ID NO:81)

ATGGAGCCCGTGGACCCCAAGCTGAAGCCCTGGAACCAACCCGGCAGCCAGCCCAAGACCGCCTGCAACAACCTGCTTCTG
CAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCCAGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCC
AGCGCCGCAGCGCCCCCCCCAGCGGCGAGGACCACCAGAACCCCTGAGCAAGCAG

FIGURE 52

FIGURE 52

>TatExon1_TV1_C_ZAw (SEQ ID NO:82)

ATGGAGCCAGTAGATCCTAAACTAAAGCCCTGGAACCATCCAGGAAGCCAACCTAAACAGCTTGTAATAATTGCTTTTG
CAAACACTGTAGCTATCATTGTCTAGTTTGCTTTCAGACAAAAGGTTTAGGCATTTCTATGGCAGGAAGAAGCGGAGAC
AGCGACGAAGCGCTCCTCCAAGTGGTGAAGATCATCAAATCCTCTATCAAAGCAG

FIGURE 53

FIGURE 53

>TatExon2_TV1_C_ZAopt (SEQ ID NO:83)

CCCCTGCCCCAGGCCCCGCGGACAGCACCGGCAGCGAGGAGAGCAAGAAGAAGGTGGAGAGCAAGACCGAGACCGACCC
CTACGACTGGTGA

FIGURE 54

FIGURE 54

>TatExon2_TV1_C_ZAw1 (SEQ ID NO:84)

CCCTTACCCCAAGCCCGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATCC
ATACGATTGGTGA

FIGURE 55

FIGURE 55

>Vif_TV1_C_ZAopt (SEQ ID NO:85)

ATGGAGAACCGCTGGCAGGTGCTGATCGTGTGGCAGGTGGACCGCATGAAGATCCGCGCCTGGAACAGCCTGGTGAAGCA
CCACATGTACATCAGCCGCCGCGCCAGCGGCTGGGTGTACCGCCACCACTTCGAGAGCCGCCACCCCAAGGTGAGCAGCG
AGGTGCACATCCCCCTGGGCGACGCCCCGCTGGTGATCAAGACCTACTGGGGCCTGCAGACCGGCGAGCGCGACTGGCAC
CTGGGCCACGGCGTGAGCATCGAGTGGCGCCTGCGCGAGTACAGCACCCAGGTGGACCCGACCTGGCCGACCAGCTGAT
CCACATGCACTACTTCGACTGCTTCACCGAGAGCGCCATCCGCCAGGCCATCCTGGGCCACATCGTGTTCCCCCGCTGCG
ACTACCAGGCCGGCCACAAGAAGGTGGGCAGCCTGCAGTACCTGGCCCTGACCGCCCTGATCAAGCCCAAGAAGCGCAAG
CCCCCCTGCCCAGCGTGCGCAAGCTGGTGGAGGACCGCTGGAACGACCCCAGAAGACCCGCGGCCGCGCGCAACCA
CACCATGAACGGCCACTAG

FIGURE 56

FIGURE 56

>Vif_TV1_C_ZAwt (SEQ ID NO:86)

ATGGAAACAGATGGCAGGTGCTGATTGTGTGGCAGGTGGACAGGATGAAGATTAGAGCATGGAATAGTTTAGTAAAGCA
CCATATGTATATATCAAGGAGAGCTAGTGGATGGGTCTACAGACATCATTTTGAAAGCAGACATCCAAAAGTAAGTTCAG
AAGTACATATCCCATAGGGGATGCTAGATTAGTAATAAAAAACATATTGGGGTTTGCAGACAGGAGAAAGAGATTGGCAT
TTGGGTCATGGAGTCTCCATAGAATGGAGACTGAGAGAATACAGCACACAAGTAGACCCTGACCTGGCAGACCAGCTAAT
TCACATGCATTATTTTGATTGTTTTACAGAATCTGCCATAAGACAAGCCATATTAGGACACATAGTTTTTCCTAGGTGTG
ACTATCAAGCAGGACATAAGAAGGTAGGATCTCTGCAATACTTGGCACTGACAGCATTGATAAAACCAAAAAAGAGAAAG
CCACCTCTGCCTAGTGTTAGAAAATTAGTAGAGGATAGATGGAACGACCCCAGAAGACCAGGGGCCGCAGAGGGAACCA
TACAATGAATGGACACTAG

FIGURE 57

105040-546660

>Vpr_TV1_C_ZAopt (SEQ ID NO:87)

ATGGAGCGCCCCCGAGGACCAGGGCCCCCAGCGCGAGCCCTACAACGAGTGGACCCTGGAGATCCTGGAGGAGCTGAA
GCAGGAGGCCGTGCGCCACTTCCCCCGCCCCTGGCTGCACAGCCTGGGCCAGTACATCTACGAGACCTACGGCGACACCT
GGACCGGCGTGGAGGCCATCATCCGCGTGCTGCAGCAGCTGCTGTTCATCCACTTCCGCATCGGCTGCCAGCACAGCCGC
ATCGGCATCCTGCGCCAGCGCCGCGCCCGCAACGGCGCCAGCCGCAGC

FIGURE 58

FIG. 58 "586660"

>Vpr_TV1_C_ZAwT (SEQ ID NO:88)

ATGGAACGACCCCCAGAAGACCAGGGGCCGCAGAGGGAACCATACAATGAATGGACACTAGAGATTCTAGAAGAACTCAA
GCAGGAAGCTGTCAGACACTTTCCTAGACCATGGCTCCATAGCTTAGGACAATATATCTATGAAACCTATGGGGATACTT
GGACGGGAGTTGAAGCTATAATAAGAGTACTGCAACAACACTACTGTTTCATTTCAGAAATTGGATGCCAACATAGCAGA
ATAGGCATCTTGCGACAGAGAAGAGCAAGAAATGGAGCCAGTAGATCC

FIGURE 59

105020"52565360

>Vpu_TV1_C_ZAopt (SEQ ID NO:89)

ATGGTGAGCCTGAGCCTGTTCAAGGGCGTGGACTACCGCCTGGGCGTGGGCGCCCTGATCGTGGCCCTGATCATCGCCAT
CATCGTGTGGACCATCGCCTACATCGAGTACCGCAAGCTGGTGCGCCAGAAGAAGATCGACTGGCTGATCAAGCGCATCC
GCGAGCGCGCCGAGGACAGCGGCAACGAGAGCGACGGCGACACCGAGGAGCTGAGCACCATGGTGGACATGGGCCACCTG
CGCCTGCTGGACGCCAACGACCTGTAA

FIGURE 60

FIGURE 60

>Vpu_TV1_C_ZAwT (SEQ ID NO:90)

ATGGTAAGTTTAAGTTTATTTAAAGGAGTAGATTATAGATTAGGAGTAGGAGCATTGATAGTAGCACTAATCATAGCAAT
AATAGTGTGGACCATAGCATATATAGAATATAGGAAATTGGTAAGACAAAAGAAAATAGACTGGTTAATTAAAAGAATTA
GGGAAAGAGCAGAAGACAGTGGCAATGAGAGTGATGGGGACACAGAAGAATTGTCAACAATGGTGGATATGGGGCATCTT
AGGCTTCTGGATGCTAATGATTGTAA

FIGURE 61

105020" 525660

dna revexon1_2TV1_C_ZAop (SEQ ID NO:91)

ATGGCCGGCCGCAGCGGCGACAGCGACGAGGCCCTGCTGCAGGTGGTGAAGATCATC
AAGATCCTGTACCAGAGCCCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCCGCCGCA
ACCGCCGCCGCCGCTGGCGCGCCCGCCAGCGCCAGATCCACACCATCGGCGAGCGCAT
CCTGGTGGCCTGCCTGGGCGCGAGCGCCGAGCCCGTGCCCCTGCAGCTGCCCCCCTG
GAGCGCCTGCACATCAACTGCAGCGAGGGCAGCGGCACCAGCGGCACCCAGCAGAGC
CAGGGCACCAACGAGGGCGTGGGCGACCCCTAA

FIGURE 62

FIGURE 62

dna Revexon1_2_TV1_C_ZAwt (SEQ ID NO:92)

ATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGCTCCTCCAAGTGGTGAAGATCATC
AAAATCCTCTATCAAAGCAACCCTTACCCCAAGCCCGAGGGGACTCGACAGGCTCGGA
GGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATCCATACGATTGGTGAGC
GGATTCTTGTCGCTTGCCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCG
CTTGAGAGACTTCATATTAATTGCAGTGAGGGCAGTGGAAGTTCTGGGACACAGCAGT
CTCAGGGGACTACAGAGGGGGTGGGAGATCCTTAA

FIGURE 63

105040" 3456860

dna TatC22Exon1_2_TV1_C_ZAopt (SEQ ID NO:93)

ATGGAGCCCGTGGACCCCAAGCTGAAGCCCTGGAACCAACCCGGCAGCCAGCCCAAG
ACCGCCGGCAACAACCTGCTTCTGCAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCC
AGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCCAGCGCCGCAGCG
CCCCCCCCAGCGGCGAGGACCACCAGAACCCCTGAGCAAGCAGCCCCTGCCCCAGGC
CCGCGGCGACAGCACCGGCAGCGAGGAGAGCAAGAAGAAGGTGGAGAGCAAGACCG
AGACCGACCCCTACGACTGGTGA

FIGURE 64

FIGURE 64

dna TatExon1_2_TV1_C_ZAwt (SEQ ID NO:95)

ATGGAGCCAGTAGATCCTAAACTAAAGCCCTGGAACCATCCAGGAAGCCAACCTAAA
ACAGCTTGTAATAATTGCTTTTGCAAACACTGTAGCTATCATTGTCTAGTTTGCTTTCA
GACAAAAGGTTTAGGCATTTCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGC
TCCTCCAAGTGGTGAAGATCATCAAATCCTCTATCAAAGCAGCCCTTACCCCAAGCC
CGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGA
GACAGATCCATACGATTGGTGA

FIGURE 66

0999575-070904
T05020" 5256660

NefD125G-Myr_TV1_C_ZAopt (SEQ ID NO:96)

ATGGCCGGCAAGTGGAGCAAGCGCAGCATCGTGGGCTGGCCCCGCGTGCGC
GAGCGCATGCGCCGCACCGAGCCCGCCGCCGAGGGCGTGGGCGCCGCCAGC
CAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCCGCCACCA
ACGAGGCCTGCGCCTGGCTGCAGGCCCCAGGAGGAGGACGGCGACGTGGGCT
TCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATGACCTACAAGAGCGCCGT
GGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCCGCAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCT
TCTTCCCCGGCTGGCAGAACTACACCAGCGGCCCCGGCGTGCGCTTCCCCCTG
ACCTTCGGCTGGTGCTTCAAGCTGGTGCCCCGTGGACCCCCGCGAGGTGAAGG
AGGCCAACGAGGGCGAGGACAACCTGCCTGCTGCACCCCATGAGCCAGCACG
GCGCCGAGGACGAGGACCGCGAGGTGCTGAAGTGGAAGTTCGACAGCCTGC
TGGCCCACCGCCACATGGCCCCGCGAGCTGCACCCCGAGTACTACAAGGACTG
CTGA

FIGURE 67

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ATGCGCGCCCGCGGCATCCTGAAGAACTACCGCCACTGGTGGATCTGGGGCATCCT
 GGGCTTCTGGATGCTGATGATGTGCAACGTGAAGGGCCTGTGGGTGACCGTGTACTA
 CGGCGTGCCCGTGGGGCCGCGAGGCCAAGACCACCTGTTCTGCGCCAGCGACGCCA
 AGGCCTACGAGAAGGAGGTGCACAACGTGTGGGGCCACCCACGCCTGCGTGCCACC
 GACCCCAACCCCCAGGAGGTGATCCTGGGCAACGTGACCGAGAACTTCAACATGTG
 GAAGAACGACATGGTGGACCAGATGCAGGAGGACATCATCAGCCTGTGGGACCAGA
 GCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGAACTGCACCAACG
 CCACCGTGAAGTACAACAACACCAGCAAGGACATGAAGAACTGCAGCTTCTACGTG
 ACCACCGAGCTGCGCGACAAGAAGAAGAAGGAGAACGCCCTGTTCTACCGCCTGGA
 CATCGTGCCCTGAACAACCGCAAGAACGGCAACATCAACAACCTACCGCCTGATCA
 ACTGCAACACCAGCGCCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGACCCCATCC
 CCATCCACTACTGCGCCCCCGCCGGCTACGCCCCCTGAAGTGCAACAACAAGAAG
 TTCAACGGCATCGGCCCTGCGACAACGTGAGCACCGTGCAGTGCACCCACGGCAT
 CAAGCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGA
 TCATCATCCGCAGCGAGAACCTGACCAACAACGTGAAGACCATCATCGTGACCTG
 AACGAGAGCATCGAGATCAAGTGACCCGCCCCGGCAACAACACCCGCAAGAGCGT
 GCGCATCGGCCCGGCCAGGCCTTCTACGCCACCGGCGACATCATCGGCGACATCC
 GCCAGGCCCACTGCAACATCAGCAAGAACGAGTGGAACACCACCCTGCAGCGCGTG
 AGCCAGAAGCTGCAGGAGCTGTTCCCCAACAGCACCGGCATCAAGTTCGCCCCCA
 CAGCGGCGGCGACCTGGAGATCACCAACCCACAGCTTCAACTGCGGCGGCGAGTTCT
 TCTACTGCAACACCACCGACCTGTTCAACAGCACCTACAGCAACGGCACCTGCACCA
 ACGGCACCTGCATGAGCAACAACACCGAGCGCATCACCTGCAGTGCCGCATCAAG
 CAGATCATCAACATGTGGCAGGAGGTGGGCCGCGCCATGTACGCCCCCCCCATCGC
 CGGCAACATCACCTGCCGAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCG
 GCGACAACAACACCGAGACCGAGACCTTCCGCCCCGGCGGCGGCGACATGCGCGAC
 AACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGGAGATCAAGCCCCTGGGCGT
 GGCCCCACCGCCGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGTGGGCA
 TCGGCGCCGTGTTCTTGGGCTTCTGGGCGCCGCCGGCAGCACCATGGGCGCCGCCA
 GCATCACCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAG
 AGCAACCTGCTGCGCGCCATCGAGGCCAGCAGCACATGCTGCAGCTGACCGTGTG
 GGGCATCAAGCAGCTGCAGGCCCGCGTGTGTCATCGAGCGCTACCTGCAGGACC
 AGCAGCTGCTGGGCCTGTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCAACGTG
 CTGTGGAACAGCAGCTGGAGCAACAAGACCCAGAGCGACATCTGGGACAACATGAC
 CTGGATGCAGTGGGACCGCGAGATCAGCAACTACACCAACACCATCTACCGCCTGC
 TGGAGGACAGCCAGAGCCAGCAGGAGCGCAACGAGAAGGACCTGCTGGCCCTGGA
 CCGCTGGAACAACCTGTGGAACCTGGTTCAGCATCACCAACTGGCTGTGGTACATCA
 GATCTTCATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCATCTTCGCCGTGCT
 GAGCCTGGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCCTGCAGACCCTGA
 TCCCCAACCCCCGCGGCCCGACCGCCTGGGCGGCATCGAGGAGGAGGGCGGCGAG
 CAGGACAGCAGCCGAGCATCCGCCTGGTGGAGCGGCTTCCTGACCCTGGCCTGGGA
 CGACCTGCGCAGCCTGTGCCTGTTCTGCTACCACCGCCTGCGCGACTTCATCCTGAT
 CGTGGTGCAGCGCCGTGGAGCTGCTGGGCCACAGCAGCCTGCGCGGCCTGCAGCGCG
 GCTGGGGCACCTGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCCTGGAGCTG
 AAGAAGAGCGCCATCAACCTGCTGGACACCATCGCCATCGCCGTGGCCGAGGGCAC
 CGACCGCATCCTGGAGTTCATCCAGAACCTGTGCCGCGGCATCCGCAACGTGCCCCG
 CCGCATCCGCCAGGGCTTCGAGGGCCGCCCTGCAGTAA

FIGURE 68

ATGAGAGCGAGGGGGATACTGAAGAATTATCGACACTGGTGGATATGGGGCATCTT
 AGGCTTTTGGATGCTAATGATGTGTAATGTGAAGGGCTTGTGGGTCACAGTCTACTA
 CGGGGTACCTGTGGGGAGAGAAGCAAAACTACTCTATTTTGTGCATCAGATGCTA
 AAGCATATGAGAAAGAAGTGCATAATGTCTGGGCTACACATGCCTGTGTACCCACA
 GACCCCAACCCACAAGAAGTGATTTTGGGCAATGTAACAGAAAATTTTAACATGTG
 GAAAAATGACATGGTGGATCAGATGCAGGAAGATATAATCAGTTTATGGGATCAAA
 GCCTTAAGCCATGTGTAAAATTGACCCCACTCTGTGTCACTTTAACTGTACAAATG
 CAACTGTTAACACTACAATAATACCTCTAAAGACATGAAAAATTGCTCTTTCTATGTAA
 CCACAGAATTAAGAGATAAGAAAAAGAAAGAAAATGCACTTTTTTATAGAÇTTGAT
 ATAGTACCACTTAATAATAGGAAGAATGGGAATATTAACAACACTATAGATTAATAAA
 TTGTAATACCTCAGCCATAACACAAGCCTGTCCAAAAGTCTCGTTTGACCCAATTCC
 TATACATTATTGTGCTCCAGCTGGTTATGCGCCTCTAAAATGTAATAATAAGAAATT
 CAATGGAATAGGACCATGCGATAATGTCAGCACAGTACAATGTACACATGGAATTA
 AGCCAGTGGTATCAACTCAATTACTGTTAATGGTAGCCTAGCAGAAGAAGAGATA
 ATAATTAGATCTGAAAATCTGACAAACAATGTCAAAACAATAATAGTACATCTTAAT
 GAATCTATAGAGATTAAATGTACAAGACCTGGCAATAATACAAGAAAGAGTGTGAG
 AATAGGACCAGGACAAGCATTCTATGCAACAGGAGACATAATAGGAGATATAAGAC
 AAGCACATTGTAACATTAGTAAAAATGAATGGAATACAACCTTTACAAAGGGTAAGT
 CAAAAATTACAAGAACTCTTCCCTAATAGTACAGGGATAAAAATTTGCACCACACTCA
 GGAGGGGACCTAGAAATTACTACACATAGCTTTAATTGTGGAGGAGAATTTTTCTAT
 TGCAATACAACAGACCTGTTTAATAGTACATACAGTAATGGTACATGCACTAATGGT
 ACATGCATGTCTAATAATACAGAGCGCATCACACTCCAATGCAGAATAAAACAAAT
 TATAAACATGTGGCAGGAGGTAGGACGAGCAATGTATGCCCCTCCCATTGCAGGAA
 ACATAACATGTAGATCAAATATTACAGGACTACTATTAACACGTGATGGAGGAGAT
 AATAATACTGAAACAGAGACATTCAGACCTGGAGGAGGAGACATGAGGGACAATTG
 GAGAAGTGAATTATATAAATACAAGGTGGTAGAAATTAAACCATTAGGAGTAGCAC
 CCACTGCTGCAAAAAGGAGAGTGGTGGAGAGAGAAAAAAGAGCAGTAGGAATAGG
 AGCTGTGTTTCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCATCAAT
 AACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAGCAAAGTA
 ATTTGCTGAGGGCTATAGAGGGCGCAACAGCATATGTTGCAACTCACGGTCTGGGGC
 ATTAAGCAGCTCCAGGCAAGAGTCCTGGCTATAGAGAGATACCTACAGGATCAACA
 GCTCCTAGGACTGTGGGGCTGCTCTGGAAAACCTCATCTGCACCACTAATGTGCTTTG
 GAACTCTAGTTGGAGTAATAAAACTCAAAGTGATATTTGGGATAACATGACCTGGAT
 GCAGTGGGATAGGGAAATTAGTAATTACACAAACACAATATACAGGTTGCTTGAAG
 ACTCGCAAAGCCAGCAGGAAAGAAATGAAAAAGATTTACTAGCATTGGACAGGTGG
 AACAATCTGTGGAATTGGTTTAGCATAACAAATTGGCTGTGGTATATAAAAAATATTC
 ATAATGATAGTAGGAGGCTTGATAGGTTTAAGAATAATTTTTGCTGTGCTCTCTCTA
 GTAAATAGAGTTAGGCAGGGATACTCACCTTGTCAATTGCAGACCCTTATCCCAAAC
 CCGAGGGGACCCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACA
 GCAGCAGATCCATTGATTAGTGAGCGGATTCTTGACACTTGCCTGGGACGACCTAC
 GAAGCCTGTGCCTCTTCTGCTACCACCGATTGAGAGACTTCATATTAATTGTAGTGA
 GAGCAGTGGAACTTCTGGGACACAGTAGTCTCAGGGGACTGCAGAGGGGGTGGGGA
 ACCCTTAAGTATTTGGGGAGTCTTGTGCAATATTGGGGTCTAGAGTTAAAAAAGAGT
 GCTATTAATCTGCTTGATACTATAGCAATAGCAGTAGCTGAAGGAACAGATAGGATT
 CTAGAATTCATACAAAACCTTTGTAGAGGTATCCGCAACGTACCTAGAAGAATAAG
 ACAGGGCTTCGAAGCAGCTTTGCAATAA

1050 54660

FIGURE 69

Gag_TV2_C_ZAopt (SEQ ID NO:99)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGGCGGCAAGCTGGACAAGTGGGAG
AAGATCCGCCTGCGCCCCGGCGGGCCGCAAGCACTACATGCTGAAGCACCTGG
TGTGGGCCAGCCGCGAGCTGGAGCGCTTCGCCGTGAACCCCGGCCTGCTGGA
GACCAGCGACGGCTGCCGCCAGATCATCAAGCAGCTGCAGCCCGCCCTGCAG
ACCGGCACCGAGGAGATCCGCAGCCTGTTCAACACCGTGGCCACCCTGTACT
GCGTGCACAAGGGCATCGACGTGCGCGACACCAAGGAGGGCCCTGGACAAGA
TCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGACCCAGCAGGCCGAGGCCG
CCGACAAGAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCC
AGATGGTGCACCAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGT
GATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTACCCGCCCTG
AGCGAGGGCGCCACCCCCCAGGACCTGAACACCATGCTGAACACCGTGGGC
GGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCC
GCCGAGTGGGACCGCCTGCACCCCGTGCACGCCGGCCCCCGTGGCCCCCGGCC
AGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCAACAGCACCCCTGCA
GGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATC
TACAAGCGCTGGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCC
CCGTGAGCATCCTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTA
CGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGAGCACCCAGGAGGTG
AAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACCCCGACTGCA
AGACCATCCTGCGCGCCCTGGGCCCCGGCGCCAGCCTGGAGGAGATGATGAC
CGCCTGCCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGCTGGCCGAG
GCCATGAGCCAGGCCAACAACACCAGCGTGATGATCCAGAAGAGCAACTTC
AAGGGCCCCCGCCGCGCCGTGAAGTGCTTCAACTGCGGCCGCGAGGGCCACA
TCGCCCCGCAACTGCCGCGCCCCCGCAAGCGCGGCTGCTGGAAGTGCGGCAA
GGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGG
CAAGATCTGGCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGC
CCCGAGCCCACCGCCCCCCCCCTGGAGCCACCGCCCCCCCCCGCCGAGAGCT
TCAAGTTCAAGGAGACCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCCTGA
CCAGCCTGAAGAGCCTGTTCGGCAGCGACCCCCTGAGCCAGTAA

FIGURE 70

Gag_TV2_C_ZAwt (SEQ ID NO:100)

ATGGGTGCGAGAGCGTCAATATTAAGAGGGGGGAAAATTAGACAAATGGGAA
AAAATTAGGTTACGGCCAGGGGGGAGAAAACACTATATGCTAAAACACCTA
GTATGGGCAAGCAGAGAGCTGGAAAGATTTGCAGTTAACCCTGGCCTTTTAG
AGACATCAGACGGATGTAGACAAATAATAAAACAGCTACAACCAGCTCTTCA
GACAGGAACAGAGGAAATTAGATCATTATTTAACACAGTAGCAACTCTCTAT
TGTGTACATAAAGGGATAGATGTACGAGACACCAAGGAAGCCTTAGACAAG
ATAGAGGAGGAACAAAACAAATGTCAGCAAAAAACACAGCAGGCGGAAGCG
GCTGACAAAAAGGTCAGTCAAAATTATCCTATAGTGCAGAACCTCCAAGGGC
AAATGGTACACCAGGCCATATCACCTAGAACCCTTGAATGCATGGGTAAAAGT
AATAGAGGAGAAGGCTTTTAGCCCAGAGGTAATACCCATGTTTACAGCATT
TCAGAAGGAGCCACCCCAACAAGATTTAAACACCATGTTAAATACAGTGGGGG
GACATCAAGCAGCCATGCAAATGTTAAAAGATACCATCAATGAGGAGGCTGC
AGAATGGGATAGGTTACATCCAGTACATGCAGGGCCTGTTGCACCAGGCCAG
ATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACACTAGTACCCTTCAA
GAACAAATAGCATGGATGACAAGTAACCCACCTATCCCAGTAGGGGGACATCT
ATAAAAGGTGGATAATTCTGGGGTTAAATAAAATAGTAAGAATGTACAGCCC
TGTCAGCATTTTAGACATAAAACAAGGACCAAAGGAACCCTTTAGAGACTAT
GTAGACCGGTTCTTCAAACTTTAAGAGCTGAACAATCTACAAGAGGTAA
AAAATTGGATGACAGACACCTTGTTAGTCCAAAATGCGAACCCAGATTGTAA
GACCATTTTAAGAGCATTAGGACCAGGGGCTTCATTAGAAGAAATGATGACA
GCATGTCAGGGAGTGGGAGGACCTAGCCACAAAGCAAGAGTTTTGGCTGAG
GCAATGAGCCAAGCAAACAATAACAAGTGTAATGATACAGAAAAGCAATTTTA
AAGGCCCTAGAAGAGCTGTTAAATGTTTCAACTGTGGCAGGGAAGGGCACAT
AGCCAGGAATTGCAGGGCCCCCTAGGAAAAGGGGCTGTTGGAAATGTGGAAA
GGAAGGACACCAAATGAAAGACTGTACTGAGAGGCAGGCTAATTTTTTAGGG
AAAATTTGGCCTTCCCAACAAGGGGAGGCCAGGGAATTCCTTCAGAGCAGAC
CAGAGCCAACAGCCCCACCACTAGAACCAACAGCCCCACCAGCAGAGAGCT
TCAAGTTCAAGGAGACTCCGAAGCAGGAGCCGAAAGACAGGGAACCTTTAA
CTTCCCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAA

FIGURE 71

Nef_TV2_C_ZAopt (SEQ ID NO:101)

ATGGGCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC
GAGCGCATCCGCCGCACCCGCAGCGCCGCCGAGGGCGTGGGCAGCGCCAGC
CAGGACCTGGAGAAGCACGGCGCCCTGACCACCAGCAACACCGCCCACAAC
AACGCCGCCTGCGCCTGGCTGGAGGCCCAGGAGGAGGAGGGCGAGGTGGGC
TTCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATGACCTACAAGGCCGCCAT
CGACCTGAGCTTCTTCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCAAGAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC
TTCTTCCCCGACTGGCAGAACTACACCCCCGGCCCCGGCGTGCGCTTCCCCCT
GACCTTCGGCTGGTACTTCAAGCTGGAGCCCGTGGACCCCCGCGAGGTGGAG
GAGGCCAACGAGGGCGAGAACAACCTGCCTGCTGCACCCCATGAGCCAGCAC
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTTCGACAGCACC
CTGGCCCGCCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACT
GCTGA

FIGURE 72

FIGURE 72

Nef_TV2_C_ZAwt (SEQ ID NO:102)

ATGGGGGGCAAGTGGTCAAAAAGCAGTATAATTGGATGGCCTGAAGTAAGA
GAAAGAATCAGACGAACTAGGTCAGCAGCAGAGGGAGTAGGATCAGCGTCT
CAAGACTTAGAGAAACATGGGGCACTTACAACCAGCAACACAGCCCACAAC
AATGCTGCTTGCGCCTGGCTGGAAGCGCAAGAGGAGGAAGGAGAAGTAGGC
TTTCCAGTCAGACCTCAGGTACCTTTAAGACCAATGACTTATAAAGCAGCAAT
AGATCTCAGCTTCTTTTTAAAAGAAAAGGGGGGACTGGAAGGGTTAATTTAC
TCCAAGAAAAGGCAAGAGATCCTTGATTTGTGGGTTTATAACACACAAGGCT
TCTTCCCTGATTGGCAAACTACACACCGGGACCAGGGGTCAGATTTCCACT
GACCTTTGGATGGTACTTCAAGCTAGAGCCAGTCGATCCAAGGGAAGTAGAA
GAGGCCAATGAAGGAGAAAACAACCTGTTTACTACACCCTATGAGCCAGCATG
GAATGGAGGATGAAGACAGAGAAGTATTAAGATGGAAGTTTGACAGTACGC
TAGCACGCAGACACATGGCCCGCGAGCTACATCCGGAGTATTACAAAGACTG
CTGA

FIGURE 73

FIGURE 73

Pol_TV2_C_ZAopt (SEQ ID NO:103)

TTCTTCCGCGAGAACCTGGCCTTCCCCAGGGCGAGGCCCGCGAGTTCCCCAGCGAGCAGACC
CGCGCCAACAGCCCCACCACCCGCACCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCAGGG
CGACAGCGAGGCCGGCGCCGAGCGCCAGGGCACCTTCAACTTCCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGCCGGCCAGACCAAGGAGGCCCTGCTGGACACCGGC
GCCGACGACACCGTGCTGGAGGAGATCAACCTGCCCGGCAAGTGGAAGCCCAAGATGATCGG
CGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCA
AGCGCGCCATCGGCACCGTGCTGGTGGGCCCCACCCCGTGAACATCATCGGCCGCAACCTGC
TGACCCAGCTGGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGC
TGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAG
GCCCTGACCGAGATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCG
AGAACCCCTACAACACCCCGTGTTCCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAG
CTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCAT
CCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCT
ACTTCAGCTGCCCCTGACGAGAGCTTCCGCAAGTACACCGCCTTACCATCCCCAGCATCA
ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC
CCCGCCATCTTCCAGAGCAGCATGACCCGCATCCTGGAGCCCTTCCGCACCCAGAACCCCGAG
GTGGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCA
CCGCGCCAAGATCGAGGAGCTGCGCGGCCACCTGCTGAAGTGGGGCTTACCACCCCCGACA
AGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGG
ACCGTGACGCCATCCAGCTGCCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCT
GGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGCATCAAGGTGCGCCAGCTGTGCA
AGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTG
GAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGCCCGTGACCGCGTGTACTACGACCCAG
CAAGGACCTGATCGCCGAGATCCAGAAGCAGGGCAACGACCAAGTGGACCTACCAGATCTACC
AGGAGCCCTTCAAGAACCTGCGCACCCGGCAAGTACGCCAAGATGCGCACCCGCCACACCAAC
GACGTGAAGCAGCTGGCCGAGGCCGTGCAGAAGATCACCCAGGAGAGCATCGTGATCTGGGG
CAAGACCCCCAAGTTCGCGCTGCCATCCCCAAGGAGACCTGGGAGACCTGGTGGAGCGACT
ACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCTGTGAACACCCCCCCCCCTGGTGAAGCTGT
GGTACCAGCTGGAGAAGGAGGCCATCGTGGGCGCCGAGACCTTCTACGTGGACGGCGCCGCC
AACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACAAGGGCCGCCAGAAGGTGG
TGAGCTTACCGGAGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAG
GACAGCGGCCCCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGC
CCAGCCCGACAAGAGCAGAGCGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAG
GAGAAGGTGTACCTGAGCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAACGAGCAGGTGGA
CAAGCTGGTGAGCAGCGGCATCCGCAAGGTGCTGTTCTTGACGGCATCGACAAGGCCCAGG
AGGAGCACGAGAAGTACCACAGCAACTGGCGCGCCATGGCCAGCGAGTTCAACCTGCCCCC
ATCGTGGCCAAGGAGATCGTGGCCAGCTGCGACAAGTGCCAGCTGAAGGGCGAGGCCATGCA
CGGCCAGGTGGACTGCAGCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGA
TCATCCTGGTGGCCGTGCACGTGGCCAGCGGCTACATGGAGGCCGAGGTGATCCCCGCCGAG
ACCGGCCAGGAGACCGCTACTTCATCCTGAAGCTGGCCGGCCGCTGGCCCGTGAAGGTGATC
CACACCGACAACGGCAGCAACTTACCAGCACCGCCGTGAAGGCCGCCTGCTGGTGGGCCGA
CATCCAGCGGAGTTCCGCATCCCCTACAACCCCCAGAGCCAGGGCGTGGTGGAGAGCATGA
ACAAGGAGCTGAAGAAGATCATCGGCCAGGTGCGCGACCAGGCCGAGCACCTGAAGACCGCC
GTGCAGATGGCCGTGTTTCATCCACAACCTTCAAGCGCAAGGGCGGCATCGGCGGCTACAGCGC
CGGCGAGCGCATCATCGACATCATCGCCAGCGACATCCAGACCAAGGAGCTGCAGAAGCAGA
TCATCAAGATCCAGAACCTCCGCGTGTACTACCGCGACAGCCGCGACCCCATCTGGAAGGGCC
CCGCCAAGCTGCTGTGGAAGGGCGAGGGCGCCGTGGTGATCCAGGACAACAGCGACATCAAG
GTGGTGCCCCGCCGCAAGGCCAAGATCATCAAGGACTACGGCAAGCAGATGGCCGGCGCCGA
CTGCGTGGCCGGCCGCCAGGACGAGGAC

FIGURE 74

Pol_TV2_C_ZAwt (SEQ ID NO:104)

TTTTTTAGGGAAAATTTGGCCTTCCCACAAGGGGAGGCCAGGGAATTCCTTCAGAGCAGACC
AGAGCCAAACAGCCCCACCACTAGAACCAACAGCCCCACCAGCAGAGAGCTTCAAGTTCAAGG
AGACTCCGAAGCAGGAGCCGAAAGACAGGGAACTTTAACTTCCCTCAAATCACTCTTTGGCA
GCGACCCCTTGTCTCAATAAAAGTAGCGGGCCAAACAAAGGAGGCTCTTTTAGATACAGGAG
CAGATGATACAGTACTAGAAGAAATAAACTTGCCAGGAAAATGGAAACCAAAAAATGATAGG
AGGAATTGGAGGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAAATTTGTGGAAA
AAGGGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTT
GACTCAGCTTGGATGCACACTAAATTTTCCAATTAGCCCCATTGAACTGTACCAGTAAAAAT
AAAGCCAGGAATGGATGGCCCAAAGGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAA
GCATTAACAGAAAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGA
AAATCCATATAACACTCCAGTATTTGCCATAAAGAAGAAGGACAGTACAAAGTGGAGAAAAAT
TAGTAGATTTTCAGGGAACTCAATAAAGAACTCAAGACTTTTGGGAAGTCCAATTAGGAATA
CCACACCCAGCAGGGTTAAAAAAGAAAAAATCAGTGACAGTACTGGATGTGGGAGATGCATA
TTTTTCAGTCCCTTTAGATGAGAGCTTCAGAAAAATATACTGCATTACCATACCTAGTATAAAC
AATGAAACACCAGGGATTAGATATCAATATAATGTTCTTCCACAGGGATGGAAAGGATCACC
AGCAATATTCCAGAGTAGCATGACAAGAATCTTAGAGCCCTTTAGAACACAAAACCCAGAAAG
TAGTTATCTATCAATATATGGATGACTTATATGTAGGATCTGACTTAGAAATAGGGCAACATA
GAGCAAAAATAGAGGAGTTAAGAGGACACCTATTGAAATGGGGATTTACCACACCAGACAAG
AAACATCAGAAAGAACCCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACA
GTACAGCCTATACAGCTGCCAGAAAAGGAGAGCTGGACTGTCAATGATATACAGAAGTTAGT
GGGAAAGTTAACTGGGCAAGTCAGATTTACCCAGGGATTAAAGTAAGGCAACTGTGTAAAC
TCCTTAGGGGAGCCAAAGCACTAACAGACATAGTGCCACTGACTGAAGAAGCAGAATTAGAA
TTGGCTGAGAACAGGGAAATTCTAAAAGAACCAGTACATGGAGTATATTATGACCCATCAAA
AGATTTAATAGCTGAAATACAGAAACAGGGGAATGACCAATGGACATATCAAATTTACCAAG
AACCATTTAAAAATCTGAGAACAGGAAAGTATGCAAAAATGAGGACTGCCACACTAATGAT
GTGAAACAGTTAGCAGAGGCAGTGCAAAAAGATAACCCAGGAAAGCATAGTAATATGGGGAA
AAACTCCTAAATTTAGACTACCCATCCCCAAAAGAAACATGGGAGACATGGTGGTCAGACTATT
GGCAAGCCACCTGGATTCCCTGAGTGGGAGTTTGTCATAACCCCTCCCCTAGTAAAATTGTGGT
ACCAGCTGGAAAAAGAACCCATAGTAGGGGCAGAAAATTTCTATGTAGATGGAGCAGCCAAT
AGGGAAACTAAAAATAGGAAAAGCAGGGTATGTCACTGACAAAGGAAGGCAGAAAGTTGTTTC
CTTCACTGAAACAACAAATCAGAAAGCTGAATTACAAGCAATTCAGCTAGCTTTGCAGGATTC
AGGGCCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAAAC
CAGATAAGAGTGAATCAGAATTAGTCAGTCAAATAATAGAACAGTTGATAAAAAAGGAAAAA
GTCTACCTATCATGGGTACCAGCACATAAAGGAATTGGAGGAAATGAACAAGTAGACAAATT
AGTAAGTAGTGGAATCAGAAAAGTACTGTTTCTAGATGGAATAGATAAAGCTCAAGAAGAGC
ATGAAAAATATCAGACGAATTGGAGAGCAATGGCTAGTGAGTTAATCTGCCACCCATAGTA
GCAAAGGAAATAGTAGCCAGCTGTGATAAATGTCAAGCTAAAAGGGGAAGCCATGCATGGACA
AGTCGACTGTAGTCCAGGAATATGGCAATTAGACTGTACACATTTAGAAGGAAAAATCATCCT
AGTAGCAGTCCATGTAGCCAGTGGCTACATGGAAGCAGAGGTTATCCCAGCAGAAACAGGAC
AAGAAACAGCATACTTTATACTAAAATTAGCAGGAAGATGGCCAGTCAAAGTAATACATACA
GATAATGGCAGTAATTTACCAGTACCGCAGTTAAGGCAGCCTGTTGGTGGGCAGATATCCAA
CGGAATTTGGAATTCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCCATGAATAAAGA
ATTAAAGAAAAATCATAGGGCAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAAA
TGGCAGTATTCATTCACAATTTTAAAAGAAAAAGGGGGGATTGGGGGGTACAGTGCAGGGGAG
AGAATAATAGACATAATAGCATCAGACATACAAATAAAGAATTACAAAACAAATTATAAAA
AATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCTATTTGGAAAGGACCAGCCAA
ACTACTCTGGAAGGTGAAGGGGCAGTAGTAATACAAGATAATAGTGATATAAAGGTAGTAC
CAAGAAGGAAAGCAAAAATCATTAAGGACTATGGAAAACAGATGGCAGGTGCTGATTGTGTG
GCAGGTAGACAGGATGAAGAT

FIGURE 75

RevExon1_TV2_C_ZAopt (SEQ ID NO:105)

ATGGCCGGCCGCAGCGGCGACAGCGACGAGGCCCTGCTGCAGGCCATCAAG
ATCATCAAGATCCTGTACCAGAGC

FIGURE 76

FIGURE 76

RevExon1_TV2_C_ZAwt (SEQ ID NO:106)

ATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGCTCCTCCAAGCAATAAAG
ATCATCAAGATCCTCTACCAAAGCA

FIGURE 77

FIGURE 77

RevExon2_TV2_C_ZAopt (SEQ ID NO:107)

CCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCCCGCCGCAACCGCCGCCGCC
GCTGGCGCGCCCGCCAGCAGCAGATCCACAGCATCAGCGAGCGCATCCTGGA
CACCTGCCTGGGCGCCCCACCAAGCCCGTGCCCTGCTGCTGCCCCCATCG
AGCGCCTGCACATCAACTGCAGCGAGAGCAGCGGCACCAGCGGCACCCAGT
AGAGCCAGGGCACCGCCGAGGGCGTGCGGCAACCCCTAA

FIGURE 78

FIGURE 78

RevExon2_TV2_C_ZAwt (SEQ ID NO:108)

ACCCTTATCCCAAACCCGAGGGGACCCGACAGGCTCGGAGGAATCGAAGAA
GAAGGTGGAGAGCAAGACAGCAGCAGATCCATTGATTAGTGAGCGGATTCT
TGACACTTGCCTGGGACGACCTACGAAGCCTGTGCCTCTTCTGCTACCACCGA
TTGAGAGACTTCATATTAATTGTAGTGAGAGCAGTGGAAGTTCTGGGACACA
GTAGTCTCAGGGGACTGCAGAGGGGGTGGGGAACCCTTAA

FIGURE 79

FIGURE 79

TatExon1_TV2_C_ZAopt (SEQ ID NO:109)

ATGGAGCCCATCGACCCCAACCTGGAGCCCTGGAACCAACCCCGGCAGCCAGC
CCAAGACCGCCTGCAACGGCTGCTACTGCAAGCGCTGCAGCTACCACTGCCT
GGTGTGCTTCCAGAAGAAGGGCCTGGGCATCTACTACGGCCGCAAGAAGCGC
CGCCAGCGCCGCAGCGCCCCCCCCCAGCAACAAGGACCACCAGGACCCCCTGC
CCAAGCAG

FIGURE 80

TatExon1_TV2_C_ZAwt (SEQ ID NO:110)

ATGGAGCCAATAGATCCTAACCTAGAACCCCTGGAACCATCCAGGAAGTCAGC
CTAAAACTGCTTGTAATGGGTGTTACTGTAAACGTTGCAGCTATCATTGTCTA
GTTTGCTTTCAGAAAAAAGGCTTAGGCATTTACTATGGCAGGAAGAAGCGGA
GACAGCGACGAAGCGCTCCTCCAAGCAATAAAGATCATCAAGATCCTCTACC
AAAGCAG

FIGURE 81

TatExon2_TV2_C_ZAopt (SEQ ID NO:111)

CCCCTGAGCCAGACCCGCGGCGACCCACCGGCAGCGAGGAGAGCAAGAAG
AAGGTGGAGAGCAAGACCGCCGCGACCCCTTCGACTAG

FIGURE 82

FIGURE 82

TatExon2_TV2_C_ZAwt (SEQ ID NO:112)

CCCTTATCCCAAACCCGAGGGGACCCGACAGGCTCGGAGGAATCGAAGAAG
AAGGTGGAGAGCAAGACAGCAGCAGATCCATTCGATTAG

FIGURE 83

FIGURE 83

Vif_TV2_C_ZAopt (SEQ ID NO:113)

ATGGAGAACCGCTGGCAGGTGCTGATCGTGTGGCAGGTGGACCGCATGAAGA
TCCGCACCTGGCACAGCCTGGTGAAGCACCACATGTACGTGAGCCGCCGCGC
CGACGGCTGGTTCTACCGCCACCACTACGAGAGCCGCCACCCCAAGGTGAGC
AGCGAGGTGCACATCCCCCTGGGCGACGCCC GCCTGGTGATCAAGACCTACT
GGGGCCTGCAGACCGGCGAGCGCGCCTGGCACCTGGGCCACGGCGTGAGCA
TCGAGTGGCGCCTGCGCCGCTACAGCACCCAGGTGGACCCCGACCTGACCGA
CCAGCTGATCCACATGCACTACTTCGACTGCTTCGCCGAGAGCGCCATCCGC -
AAGGCCATCCTGGGCCAGATCGTGAGCCCCAAGTGCGACTACCAGGCCGGCC
ACAACAAGGTGGGCAGCCTGCAGTACCTGGCCCTGACCGCCCTGATCAAGCC
CAAGAAGATCAAGCCCCCCTGCCAGCGTGCGCAAGCTGGTGGAGGACCGC
TGGAACAAGCCCCAGAAGACCCGCGGCCGCCGCGGCAACCACACCATGAAC
GGCCACTAG

FIGURE 84

105040" 54366660

Vif_TV2_C_ZAwt (SEQ ID NO:114)

ATGGAAAACAGATGGCAGGTGCTGATTGTGTGGCAGGTAGACAGGATGAAG
ATTAGAACATGGCACAGTTTAGTAAAGCACCATATGTATGTTTCGAGGAGAG
CTGATGGATGGTTCTACAGACATCATTATGAAAGCAGACACCCAAAAGTAAG
TTCAGAAGTACACATCCCATTAGGAGATGCCAGGTTAGTAATAAAAACATAT
TGGGGTCTGCAGACAGGAGAAAGAGCTTGGCATTGTTGGGTACGGAGTCTCCA
TAGAATGGAGATTGAGAAGATATAGCACACAAGTAGACCCTGACCTGACAG
ACCAACTAATTCATATGCATTATTTTGATTGTTTTGCAGAATCTGCCATAAGG-
AAAGCCATACTAGGACAGATAGTTAGCCCTAAGTGTGACTATCAAGCAGGAC
ATAACAAGGTAGGATCTCTACAATACTTGGCACTGACAGCATTGATAAAACC
AAAAAAGATAAAGCCACCTCTGCCTAGTGTTAGGAAATTAGTAGAGGATAGA
TGGAACAAGCCCCAGAAGACCAGGGGCCGCAGAGGGAACCATACAATGAAT
GGACACTAG

FIGURE 85

105040 5256660

Vpr_TV2_C_ZAopt (SEQ ID NO:115)

ATGGAGCAGGCCCCGAGGACCAGGGCCCCCAGCGCGAGCCCTACAACGAG
TGGACCCTGGAGCTGCTGGAGGAGCTGAAGCAGGAGGCCGTGCGCCACTTCC
CCCGCCCCCTGGCTGCACAACCTGGGGCCAGCACATCTACGAGACCTACGGCGA
CACCTGGACCGGCGTGGAGGCCATCATCCGCATCCTGCAGCAGCTGCTGTTC
ATCCACTTCCGCATCGGCTGCCACCACAGCCGCATCGGCATCCTGCGCCAGC
GCCGCGCCCGCAACGGCGCCAACCGCAGC

FIGURE 86

FIGURE 86

Vpr_TV2_C_ZAwt (SEQ ID NO:116)

ATGGAACAAGCCCCAGAAGACCAGGGGCCGCAGAGGGAACCATACAATGAA
TGGACACTAGAGCTTTTAGAAGAACTCAAGCAGGAAGCTGTCAGACACTTTC
CTAGACCATGGCTCCATAACTTAGGACAACATATCTATGAAACCTATGGAGA
TACTTGGACAGGAGTTGAAGCAATAATAAGAATCCTGCAACAATTACTGTTT
ATTCATTTTCAGGATTGGGTGCCATCATAGCAGAATAGGCATTTTGCGACAGA
GAAGAGCAAGAAATGGAGCCAATAGATCC

FIGURE 87

Vpu_TV2_C_ZAopt (SEQ ID NO:117)

ATGCTGGACCTGACCGCCCGCATCGACAGCCGCCTGGGCATCGGCGCCCTGA
TCGTGGCCCTGATCATCGCCATCATCGTGTGGACCATCGTGTACATCGAGTAC
CGCAAGCTGGTGCGCCAGCGCAAGATCGACTGGCTGGTGAAGCGCATCCGCG
AGCGCGCCGAGGACAGCGGCAACGAGAGCGAGGGCGACACCGAGGAGCTGA
GCACCCTGGTGGACATGGGGCACCTGCGCCTGCTGGACGCCAACGACGTGTA
A

FIGURE 88

FIGURE 88

Vpu_TV2_C_ZAwt (SEQ ID NO:118)

ATGTTAGATTTAAGTCAAGAATAGATTCTAGATTAGGAATAGGAGCATTGA
TAGTAGCACTAATCATAGCAATAATAGTGTGGACCATAGTATATATAGAATA
TAGGAAATTGGTAAGGCAAAGGAAAATAGACTGGTTAGTTAAAAGGATTAG
GGAAAGAGCAGAAGACAGTGGCAATGAGAGCGAGGGGGATACTGAAGAATT
ATCGACACTGGTGGATATGGGGCATCTTAGGCTTTTGGATGCTAATGATGTGT
AA

FIGURE 89

099957-070504

gp120mod.TV1.delV2 (SEQ ID NO:119)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctggggcatc
61 ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
121 ggcgtgcccg tgtggcgcca cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct gcgtgcccac cgaccccaac
241 cccagggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgaccc ccctgtgcgt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcacttaca catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgca caccagcacc
541 atcaccagg cctgccccaa ggtgagcttc gacccatcc ccatccacta ctgcgcccc
601 gccggctacg ccatcctgaa gtgcaacaac aagaccttca acggcaccgg ccctgctac
661 aacgtgagca ccgtgcagtg caccacggc atcaagcccg tggtagcac ccagctgctg
721 ctgaacggca gcctggccga ggagggcatc atcatccgca gcgagaacct gaccgagaac
781 accaagacca tcactgtgca cctgaacgag agcgtggaga tcaactgcac ccgccccaa
841 aacaacacc gcaagagcgt gcgcacggc ccggccagg cttctacgc caccaacgac
901 gtgatcgga acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttccca acaagaccat ccagttaag
1021 cccacgccg gcggcgacct ggagatcacc atgcacagct tcaactgccg cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaaaa cggcacctac
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcattgtgc agggcggtgg ccaggccacc tacgcccccc ccacgcccgg caacatcacc
1261 tggcgagca acatcaccgg catcctgctg acccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga ccttcgccc cgccggcggc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtggtgga gatcaagccc ctgggcatcg ccccaacaa ggccaagcgc
1441 cgcgtggtgc agcgcgagaa gcgctaactc gag

FIGURE 90

```

1  gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctgggggcac
61  ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
121 ggcgtgcccg tgtggcgcgga cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtggggc acccacgcct gcgtgcccac cgaccccaac
241 cccagaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtggggacc agagcctgaa gccctgctg
361 aagctgaccc ccctgtgcgt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcactctaaa catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc
541 atcaccaggg cctgccccaa ggtgagcttc gaccccatcc ccatccacta ctgcgcccc
601 gccggctacg ccatcctgaa gtgcaacaac aagaccttca acggcaccgg cccctgctac
661 aacgtgagca ccgtgcagtg caccacggcg atcaagcccc tgggtgagcac ccagctgctg
721 ctgaacggga gcctggccga ggagggcac atcatccgca gcgagaacct gaccgagaac
781 accaagacca tcatcgtgca cctgaacgag agcgtggaga tcaactgcac ccgccccaac
841 aacaacaccc gcaagagcgt gcgcatcgcc cccggccagg ccttctacgc caccaacgac
901 gtgatcggga acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttcccc acaagaccat ccagttcaag
1021 cccacgcgg gcggcgacct ggagatcacc atgcacagct tcaactgcgg cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcgtgtggc agggcggtgg ccaggccacc tacgcccccc ccatcgccgg caacatcacc
1261 tgccgcagca acatcaccgg catcctgctg acccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga ccttccgccc cggcgggcgg gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtggtgga gatcaagccc ctgggcatcg cccccaccaa ggccaagcgc
1441 cgcgtggtgc agcgcgagaa gcgcgccgtg ggcacgcggc ccgtgttcct gggcttcctg
1501 ggcgcgcgg gcagcaccat gggcgccgcc agcatcacc tgaccgtgca ggcccgcag
1561 ctgctgagcg gcacgtgca gcagcagagc aacctgctga aggccatcga ggcccagcag
1621 cacatgctgc agctgaccgt gtggggcatc aagcagctgc agggccgcgt gctggccatc
1681 gagcgctacc tgaaggacca gcagctgctg ggcacatggg gctgcagcgg ccgcctgac
1741 tgcaccaccg ccgtgccttg gaacagcagc tggagcaaca agagcgagaa ggacatctgg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagcca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921 gacaagtgga acaacctgtg gaactggttc gacatcagca actggccctg gtacatctaa
1981 ctcgag

```

FIGURE 91

gp140mod.TV1.mut7.delV2 (SEQ ID NO:121)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtggtggat ctggggcadc
61 ctgggcttct ggatgctgat gatctgaac accgaggacc tgtgggtgac cgtgtactac
121 ggcgtgcccg tgtggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct gcgtgcccac cgaccccaac
241 ccccaggaga tcgtgctggg caactgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgacc cctgtgcgt gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcacttaca catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc
541 atcaccagg cctgccccaa ggtgagcttc gacccatcc ccatccacta ctgcgcccc
601 gccggtacg ccatcctgaa gtgcaacaac aagaccttca acggcaccgg cccctgctac
661 aacgtgagca ccgtgcagt caccacggc atcaagccc tggtgagcac ccagtctgtg
721 ctgaacggca gcctggccga ggagggcac atcatccga gcgagaacct gaccgagaac
781 accaagacca tcatcgtgca cctgaacgag agcgtggaga tcaactgac cgccccaac
841 aacaacacc gcaagagcgt gcgcatcgcc cccggccagg ccttctacgc caccaacgac
901 gtgatcggca acatccgca ggccactgc aacatcagca ccgaccgtg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttccca acaagaccat ccagtcaag
1021 ccccacgcc gcggcgacct ggagatcacc atgcacagct tcaactccg cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaaaa cggcacctac
1141 aagtacaac gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcatgtggc agggcgtggg ccaggccacc tacgcccc ccatcgccgg caacatcacc
1261 tgccgcagca acatcaccgg catctgtg acccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga cttccgccc cggcgccggc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca agtggtgga gatcaagccc ctgggcatcg cccccacaa ggccatcagc
1441 agcgtggtgc agagcgagaa gagcgccgtg ggcatcgcg ccgtgttctt gggcttctg
1501 ggcgcccgcg gcagcaccat gggcgccgc agcatcacc tgaccgtgca ggcccgccag
1561 ctgctgagcg gcacgtgca gcagcagagc aacctgctga aggccatcga ggccagcag
1621 cacatgctgc agctgaccgt gtggggcadc aagcagctgc agggccgct gctggccatc
1681 gagcgtacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgcctgac
1741 tgcaccaccg ccgtgccctg gaacagcagc tggagcaaca agagcgagaa ggacatctg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagca gaaccagcag gagaagaac agaaggacct gctggagctg
1921 gacaagtga acaacctgtg gaactggttc gacatcagca actggccctg gtacatctaa
1981 ctcgag

FIGURE 92

gp160mod.TV1.delV1V2 (SEQ ID NO:122)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtgat ctggggcadc
61 ctgggcttct ggatgtgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
121 ggctgtcccc tgtggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgcccac cgaccccaac
241 cccagaggaga tcgtgtggg caactgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gcctgtcgtg
361 aagctgacc cctgtgcgt gggcgccggc aactgcaaca ccagcaccat caccagggc
421 tgcccaagg tgagcttga cccatcccc atccactact gcgccccgc cggctacgcc
481 atcctgaagt gcaacaacaa gaccttcaac ggcaccggcc cctgtacaa cgtgagcacc
541 gtgcagtga cccacggcat caagcccgtg gtgagcacc agctgtgtgt gaacggcagc
601 ctggccgagg agggcatcat catccgagc gagaacctga ccgagaacac caagaccatc
661 atcgtgcacc tgaacgagag cgtggagatc aactgcacc gccccaacaa caacaccgc
721 aagagcgtgc gcatcgccc cggccaggcc ttctacgcca ccaacgacgt gatcggcaac
781 atccgccagg cccactgaa catcagcacc gaccgtgga acaagacct gcagcagggtg
841 atgaagaagc tggcgagca ctccccaac aagaccatcc agttcaagcc ccacgccggc
901 ggcgacctgg agatccat gcacagctt aactgccgcg gcgagttct ctactgcaac
961 accagcaacc tgttaacag cacctaccac agcaacaac gcacctaaa gtacaacggc
1021 aacagcagca gcccacac cctgcagtgc aagatcaagc agatcgtgc catgtggcag
1081 ggctgtggcc agggcaccta cggcccccc atcgccggca acatcacctg ccgagcaac
1141 ataccggca tctgtgtac ccgcgacggc ggcttcaaca ccaccaaaa caccgagacc
1201 ttccgcccc gcggcgccga catgcgcgac aactggcgca gcgagctgta caagtacaag
1261 gtggtggaga tcaagcccct gggcatcgcc cccaccaagg ccaagcgccg cgtggtgcag
1321 cgcgagaagc gcgccgtgg catcgccgc gtgttcttg gttcttggt cgcgcggc
1381 agcaccatgg gcgccccag catcacctg accgtgcagg cccgccagct gctgagcggc
1441 atcgtgcagc agcagagcaa cctgtgaag gccatcgagg cccagcagca catgtgcag
1501 ctgaccgtgt ggggcatcaa gcagctgcag gcccgctgc tggccatga gcgtacctg
1561 aaggaccagc agctgtgtgg catctggggc tgcagcgcc gcctgatctg caccaccgc
1621 gtgccctgga acagcagctg gagcaacaag agcgagaagg acatctggga caacatgacc
1681 tggatgcagt gggaccgca gatcagcaac tacaccggcc tgatctaaa cctgtggag
1741 gacagccaga accagcagga gaagaacgag aaggacctgc tggagctga caagtgaac
1801 aacctgtgga actggttga catcagcaac tggccctggt acatcaagat ctctcatg
1861 atcgtggcg gcctgatcg cctgcgcatc atctcgccg tgctgagcat cgtgaaccg
1921 gtgcgccagg gctacagccc cctgagctt cagacctga ccccagccc ccgcggcctg
1981 gaccgctgg gcggcatga ggaggaggc ggcgagcagg accgcgacc cagcatccg
2041 ctggtgagc gttctgag cctggcctg gacgacctg gcaacctgt cctgttcag
2101 taccaccgc tgcgcgact catctgatc gccgtgcgc cgtggagct gctgggccac
2161 agcagcctgc gcggcctga gcgcggctg gagatctga agtacctgg cagcctggtg
2221 cagtactgg gcctggagct gaagaagag gccatcagc tctggacac catcgccatc
2281 accgtggccg agggcaccga ccgcatcatc gagctggtg agcgcatct ccgcgccatc
2341 ctgaacatcc cccgccgat ccgccaggc ttcgaggcc cctgtgtga actcgag

FIGURE 93

gp160mod.TV1.delV2 (SEQ ID NO:123)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctggggcatc
61 ctgggcttct ggatgctgat gatctgaac accgaggacc tgtgggtgac cgtgtactac
121 ggcggtgcccc tgtggcgcca cgccaagacc accctgttct gcgccagcca cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct gcgtgcccac cgaccccaac
241 cccagaggaga tcgtgctggg caactgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgacc cctgtgcgt gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcacttaca catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc
541 atcaccagg cctgccccaa ggtgagcttc gacctatcc ccattcacta ctgcgcccc
601 gccggtacg ccactctgaa gtgcaacaac aagacctta acggcaccgg cccctgctac
661 aacgtgagca ccgtgcagt caccacggc atcaagccc tggtgagcac ccagctgctg
721 ctgaacggca gcctggcca ggagggcac atcatccga gcgagaacct gaccgagaac
781 accaagacca tcatctgca cctgaacgag agcgtggaga tcaactgcac cgccccaac
841 aacaacacc gcaagagcgt gcgcatcggc cccggccagg ccttctacgc caccaacgac
901 gtgatcggca acatccgcca ggcccactgc aacatcagca ccgaccgtg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttccca acaagaccat ccagttcaag
1021 cccacgccg gcggcgacct ggagatcacc atgcacagct tcaactgcc cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaaaa cggcacctac
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcattgtgc agggcggtgg ccaggccacc tacgcccccc ccactgccgg caacatcacc
1261 tgccgcagca acatcaccgg catctgctg acccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga ccttcgccc cggcggcggc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtgtgga gatcaagccc ctgggcatcg ccccccacaa ggccaagcgc
1441 cgcgtgtgac agcgcgagaa gcgcgccgtg ggcatcggcg cctgttctt gggttctctg
1501 ggcgccgccg gcagcaccat gggcgccgcc agcatcacc tgaccgtgca ggcccggcag
1561 ctgctgagcg gcactgtgca gcagcagagc aacctgtga aggccatga ggcccagcag
1621 cacatgctgc agctgaccgt gtggggcatc aagcagctgc agggccgct gctggccatc
1681 gagcgctacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgcctgac
1741 tgcaccaccg ccgtgccctg gaacagcagc tggagcaaca agagcgagaa ggacatctgg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagcca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921 gacaagtga acaacctgtg gaactggttc gacatcagca actggccctg gtacatcaag
1981 atcttcatca tgatcgtgg cgccctgatc ggctgcgca tcatctcgc cgtgctgagc
2041 atcgtgaacc gcgtgcgcca gggtacagc cccctgagct tccagacct gacccaccg
2101 cccgcgggcc tggaccgct gggcggcatc gaggaggagg gcggcgagca ggaccgcgac
2161 cgcagcatcc gcctggtgag cggcttctg agcctggcct gggacgacct gcgcaacctg
2221 tgcctgttca gtaccaccg cctgcgcgac ttatctctga tcgccgtgc cgccgtggag
2281 ctgctgggcc acagcagcct gcgcggcctg cagcgcggct gggagatcct gaagtacctg
2341 ggagcctgg tgactactg ggccctggag ctgaagaaga gcgccatcag cctgctggac
2401 accatcgcca taccgtggc cgagggcacc gaccgatca tcgagctggt gcagcgcac
2461 tgccgcgcca tctgaacat ccccgccgc atccgccagg gcttcgaggc cgccctgctg
2521 taactcag

FIGURE 94

gp160mod.TV1.mut7.delV2 (SEQ ID NO:124)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtggtggat ctggggcatc
61 ctgggcttct g gatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
121 ggcggtcccc tgtggcgga cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct gcgtgcccac cgaccccaac
241 cccagggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtggggacc agagcctgaa gccctgcgtg
361 aagctgacct ccctgtgcgt gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcacttacia catcgaggag
481 atgaagaact gcagcttcaa gcgcggcgcc ggccgctga tcaactgcaa caccagcacc
541 atcaccagg cctgccccaa ggtgagcttc gacccatcc ccatccacta ctgcgcccc
601 gccggctacg ccactctgaa gtgcaacaac aagaccttca acggcaccgg cccctgctac
661 aacgtgagca ccgtgcagtg caccacggc atcaagcccg tggtagcac ccagctgctg
721 ctgaacggca gcctggccga ggagggcac atcatccga gcgagaacct gaccgagaac
781 accaagacca tcactgtgca cctgaacgag agcgtggaga tcaactgcac ccgccccaac
841 aacaacacc gcaagagcgt gcgcatcggc cccggccagg ccttctacgc caccaacgac
901 gtgatcggca acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttccca acaagaccat ccagttcaag
1021 cccacgcgg gcggcgacct ggagatcacc atgcacagct tcaactgcc cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcattgtggc agggcggtgg ccaggccacc tacgcccccc ccactgccgg caacatcacc
1261 tgccgcagca acatcaccgg catctgctg accgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga ccttcgccc cggcggcgcc gacatgcgag acaactggcg cagcgagctg
1381 tacaagtaca aggtggtgga gatcaagccc ctgggcatcg cccccacca ggccatcagc
1441 agcgtggtgc agagcgagaa gagcgccgtg ggcatcggcg ccgtgttctt gggcttctg
1501 ggcgccgccc gcagcaccat gggcgccgcc agcatcacc tgaccgtgca ggcccggcag
1561 ctgctgagcg gcactgtgca gcagcagagc aacctgctga aggccatcga ggcccagcag
1621 cacatgctgc agctgaccgt gtggggcatc aagcagctgc agggccgct gctggccatc
1681 gagcgctacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgctgac
1741 tgcaccaccg ccgtgccctg gaacagcagc tggagcaaca agagcgagaa ggacatctgg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagcca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921 gacaagtgga acaacctgtg gaactggttc gacatcagca actggccctg gtacatcaag
1981 atcttcatca tgatcgtggg cggcctgac ggccctgcga tcactctgc cgtgctgagc
2041 atcgtgaacc gcgtgcgcca gggctacagc cccctgagct tccagacct gacccccagc
2101 cccgcggcc tggaccgctt gggcgccatc gaggaggagg gcggcgagca ggaccgcgac
2161 cgcagcatcc gcctggtgag cggcttctg agcctggcct gggacgacct gcgcaacctg
2221 tgcctgttca gctaccaccg cctgcgcgac ttcactctga tcgccgtgc cgccgtggag
2281 ctgctgggcc acagcagcct gcgcggcctg cagcgcggct gggagatcct gaagtacctg
2341 ggcagcctgg tcagttactg gggcctggag ctgaagaaga gcgccatcag cctgctggac
2401 accatcgcca tcacctggc cgagggcacc gaccgcatca tcgagctggt gcagcgcac
2461 tgccgcgcca tctgaacat ccccgccgc atccgccagg gcttcgaggc cgccctgctg
2521 taactcgag

FIGURE 95

gp160mod.TV1.tpa1 (SEQ ID NO:125)

1 gtcgacgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga
 61 gcagtcttcg ttgcgccag cgccagcacc gaggacctgt gggtgaccgt gtactacggc
 121 gtgcccgtgt ggcgcgacgc caagaccacc ctgttctgcg ccagcgacgc caaggcctac
 181 gagaccgagg tgcacaacgt gtgggccacc cagcctgcg tgcccaccga cccaacccc
 241 caggagatcg tgctgggcaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggcc
 301 gaccagatgc acgaggacgt gatcagcctg tgggaccaga gcctgaagcc ctgcgtgaag
 361 ctgaccccc tgtgcgtgac cctgaactgc accgacacca acgtgaccgg caaccgcacc
 421 gtgaccggca acagcaccaa caacaccaac ggcaccggca tctacaacat cgaggagatg
 481 aagaactgca gcttcaacgc caccaccgag ctgcgcgaca agaagcaca ggagtacgcc
 541 ctgttctacc gcctggacat cgtgcccctg aacgagaaca gcgacaactt cacctaccgc
 601 ctgatcaact gcaacaccag caccatcacc caggcctgcc ccaagtgtag cttcgacccc
 661 atccccatcc actactgcgc cccgcgcggc tacgccatcc tgaagtgcaa caacaagacc
 721 ttaacggca cgggccctg ctacaacgtg agcaccgtgc agtgaccca cggcataag
 781 cccgtggtga gcaccagct gctgctgaac ggcagcctgg ccgaggaggg catcatcatc
 841 cgcagcgaga acctgaccga gaacaccaag accatcatcg tgcacctgaa cgagagcgtg
 901 gagatcaact gcaccgccc caacaacaac acccgcaaga gcgtgcgcat cggccccggc
 961 caggccttct acgccacaa cgacgtgatc ggcaacatcc gccaggccca ctgcaacatc
 1021 agcaccgacc gctggaacaa gacctgcag cagggtgatga agaagctggg cgagcacttc
 1081 cccaacaaga ccatccagtt caagccccac gccggcgcg acctgagat caccatgcac
 1141 agcttcaact gccgcggcga gttctctac tgcaacacca gcaacctgtt caacagcacc
 1201 taccacagca acaacggcac ctacaagtac aacggcaaca gcagcagccc catcacctg
 1261 cagtgaaga tcaagcagat cgtgcgcatg tggcagggcg tgggccaggc cacctacgcc
 1321 cccccatcg ccggcaacat cacttgccgc agcaacatca ccggcatcct gctgaccgc
 1381 gacggcggt tcaacaccac caacaacacc gagaccttc gccccggcg cgcgacatg
 1441 cgcgacaact ggcgacgca gctgtacaag tacaaggtgg tgagatcaa gccctgggc
 1501 atgccccca ccaaggccaa gcgcccgtg gtgcagcgcg agaagcgcg cgtgggcatc
 1561 ggcgccgtgt tcttgggctt cctggggccc gccggcagca ccatgggcgc cgccagcatc
 1621 acctgaccg tcaggcccc ccagctgctg agcggcatcg tgcagcagca gagcaacctg
 1681 ctgaaggcca tcaggccca gcagcacatg ctgcagctga ccgtgtgggg catcaagcag
 1741 ctgcaggccc gcgtgtggc catcgagcg tacttgaagg accagcagct gctgggcatc
 1801 tggggctgca gcggccgct gatctgcacc accgccgtgc cctggaacag cagctggagc
 1861 aacaagagcg agaaggacat ctgggacaac atgacctgga tgcaatggga ccgcgagatc
 1921 agcaactaca ccggcctgat ctacaactg ctggaggaca gccagaacca gcaggagaag
 1981 aacgagaagg acctgctgga gctggacaag tggaacaacc tgtggaactg gtgcacatc
 2041 agcaactggc cctggtacat caagatcttc atcatgatcg tggcgggcct gatcggcctg
 2101 cgcatcatct tcgccgtgct gagcatcgtg aaccgcgtgc gccagggcta cagccccctg
 2161 agcttcaga cctgacccc cagccccgc gccctggacc gcctgggcgg catcgaggag
 2221 gagggcgcg agcaggaccg cgaccgcagc atccgcctgg tgagcggtt cctgagcctg
 2281 gcctgggacg acctgcgcaa cctgtgcctg ttacgtacc accgcctgcg cgacttcate
 2341 ctgatcgccg tgcgcgccgt ggagctgctg ggccacagca gcctgcgcgg cctgcagcgc
 2401 ggctgggaga tctgaagta cctgggcagc ctggtgcagt actggggcct ggagctgaag
 2461 aagagcgcca tcagcctgct ggacaccatc gccatcaccg tggccgaggg caccgaccgc
 2521 atcatcgagc tgggtgcagc catctgccgc gccatcctga acatccccg ccgcatccgc
 2581 cagggttcg aggcgcctt gctgtaact gag

FIGURE 96

1 gaattcatgc gctgatggg caccagaag aactgccagc agtgggtgat ctggggcatc
 61 ctgggcttct g gatgctgat gatctcaac accgaggacc tgtgggtgac cgtgtactac
 121 ggctgccccg tgtggcgga cgcaagacc accctgttct gcgccagcga cgcaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgccac cgacccaac
 241 cccaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
 301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgacct cctgtgctg gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag
 481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtac
 541 gccctgttct accgcctgga catcgtgccc ctgaacgaga acagcgacaa cttcacctac
 601 cgctgatca actgcaacac cagcaccatc acccaggcct gcccgaagt gagcttcgac
 661 cccatcccca tccactactg cgccccgcc ggctacgcca tctgaagtg caacaacaag
 721 acctcaacg gcaccggccc ctgtacaac gtgagcaccg tgcagtgcac ccacggcatc
 781 aagcccgctg tgagcaccca gctgctgtg aacggcagcc tggccgagga gggcatcatc
 841 atccgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
 901 gtggagatca actgaccccg cccaacaac aacaccgca agagcgtgcg catcggcccc
 961 ggccaggcct tctagccac caacgacgtg atcggaaca tccgccagc cactgcaac
 1021 atcagcaccg accgctggaa caagacctg cagcaggtga tgaagaagct gggcgagcac
 1081 tccccaaac agaccatcca gttcaagccc cagccggcg gcgacctgga gatcaccatg
 1141 cacagcttca actgccgagg cgagtcttc tactgcaaca ccagcaacct gttcaacagc
 1201 acctaccaca gcaacaacgg cacctacaag tacaacggca acagcagcag ccccatcacc
 1261 ctgcagtgca agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
 1321 gccccccca tcgccggcaa catcacctgc cgcagcaaca tcaccggcat cctgctgacc
 1381 cgcgacggcg gttcaacac caccaacaac accgagacct tccgccccgg cggcggcgac
 1441 atgcgcgaca actggcgagc cgagctgtac aagtacaagg tgggtggagat caagcccctg
 1501 ggcacgccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg cgccgtgggc
 1561 atcgcgccg tgttctggg ctctctgggc gccgccggca gcaccatggg cgccgccagc
 1621 atcacctga ccgtgcagcg ccgccagctg ctgagcgga tcgtgcagca gcagagcaac
 1681 ctgtgaagg ccatcgaggc ccagcagcac atgtgcagc tgaccgtgtg gggcatcaag
 1741 cagctgcagg ccgcgtgct ggccatcgag cgctacctga aggaccagca gctgctgggc
 1801 atctgggct gcagcgccg cctgatctgc accaccgccc tgcctggaa cagcagctgg
 1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
 1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
 1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtggaa ctggttcgac
 2041 atcagcaact ggccctggtg catcaagatc tcatcatga tcgtgggagg cctgatcggc
 2101 ctgcgcatca tcttcgccg gctgagcatc gtgaaccgcg tgcgccaggg ctacagcccc
 2161 ctgagcttcc agacctgac cccagcccc cgcggcctgg accgcctggg cggcatcgag
 2221 gaggagggcg gcgagcagga ccgcgaccgc agcatccgc tggtagcgg ctctctgagc
 2281 ctggcctggg acgacctgcg caacctgtgc ctgttcagct accaccgct gcgcgacttc
 2341 atctgatcg ccgtgcgcgc cgtggagctg ctgggccaca gcagcctgcg cggcctgcag
 2401 cgcggctggg agatctgaa gtacctgggc agcctggtgc agtactggg cctggagctg
 2461 aagaagagcg ccatcagcct gctggacacc atgccatca ccgtggccga gggcaccgac
 2521 cgcatcatcg agctggtgca gcgcatctgc cgcgccatcc tgaacatccc ccgccgcatc
 2581 cgccagggct tcgaggccgc cctgctgtaa ctcgag

FIGURE 97

1 gaattcatga gagtgatggg gacacagaag aattgtcaac aatggtggat atggggcatc
 61 ttaggcttct ggatgctaata gatttgaac accgaggacc tgtgggtgac cgtgtactac
 121 ggcggtgccc tgtggcgcca cgccaagacc accctgttct gcgccagcga cgccaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgccac cgacccaac
 241 cccaggaga tcgtgtggg caacgtgacc gagaactca acatgtggaa gaacgacatg
 301 gccgaccaga tgcacagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgacc ccctgtgct gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgacc gcaacagcac caacaacacc aacggcaccg gcatctacaa catcaggag
 481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtac
 541 gccctgttct accgctgga catcgtgcc ctgaacgaga acagcgacaa cttcacctac
 601 cgctgatca actgcaacac cagcaccatc acccaggcct gccccagggt gagcttcgac
 661 cccatcccca tccactactg ccccccgcc ggctacgcca tctgaagtg caacaacaag
 721 acctcaacg gcaccggccc ctgctacaac gtgagcaccg tgcagtgcac ccacggcatc
 781 aagcccgtgg tgagcaccga gctgctgctg aacggcagcc tggccgagga gggcatcatc
 841 atccgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
 901 gtggagatca actgacccc cccaacaac aacaccgcga agagcgtgcg catcggcccc
 961 ggccaggcct tctacgccac caacgacgtg atcggcaaca tccgccagge ccaactgcaac
 1021 atcagcaccg accgctggaa caagaccctg cagcagggtga tgaagaagct gggcgagcac
 1081 tccccaaaca agaccatcca gttcaagccc cagccggcg gcgacctgga gatcaccatg
 1141 cacagcttca actgccggcg cgagttctt tactgcaaca ccagcaacct gttcaacagc
 1201 acctaccaca gcaacaacgg cacctacaag tacaacggca acagcagcag ccccatcacc
 1261 ctgcagtga agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
 1321 gccccccca tcgccggcaa catcactgc cgcagcaaca tcaccggcat cctgtgacc
 1381 cgcgacggcg gttcaacac caccaacaac accgagacct tccgccccg cggcgcgagc
 1441 atgcgcgaca actggcgag cgagctgtac aagtacaagg tggtaggat caagccctg
 1501 ggcacgccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg cgccgtgggc
 1561 atcggcgccg tgttctggg ctctctggg gccgccggca gcacctggg cgccgccagc
 1621 atcacctga ccgtgcaggc ccgccagctg ctgagcggca tcgtgcagca gcagagcaac
 1681 ctgctgaagg ccatcgaggc ccagcagcac atgctgcagc tgacctgtg gggcatcaag
 1741 cagctgcagg ccgcgtgct ggccatcgag cgctacctga aggaccagca gctgctgggc
 1801 atctggggct gcagcgcccg cctgatctgc accaccgccc tgccttgaa cagcagctgg
 1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
 1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
 1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtgaa ctggttcgac
 2041 atcagcaact ggccctggta catcaagatc ttcacatga tcgtgggccc cctgatcgcc
 2101 ctgcgcatca tcttcgccgt gctgagcatc gtgaaccgcg tgcgccaggg ctacagcccc
 2161 ctgagcttcc agacctgac cccagcccc cgcggcctgg accgctggg cggcacgag
 2221 gaggagggcg gcgagcagga ccgcgaccgc agcatccgcc tggtagcgg ctctctgagc
 2281 ctggcctggg acgacctgc caacctgtgc ctgttcagct accaccgct gcgcgacttc
 2341 atcctgatcg ccgtgcgcgc cgtggagctg ctgggccaca gcacctgcg cggcctgcag
 2401 cgcggctggg agatctgaa gtacctgggc agcctggtgc agtactggg cctggagctg
 2461 aagaagagcg ccatcagcct gctggacacc atcgccatca ccgtggccga gggcaccgac
 2521 cgcatcatcg agctggtgca gcgcatctgc cgcgccatcc tgaacatccc ccgccgcatc
 2581 cgccagggtc tcgaggccgc cctgctgtaa ctgag

FIGURE 98

Wild-type Env gp160 (8_2_ZA) (SEQ ID NO:128)

1 atgagagtga tggggacaca gaagaattgt caacaatggt ggatatgggg catcttaggc
61 ttctggatgc taatgatttg taacacggag gacttgtggg tcacagtcta ctatggggta
121 cctgtgtgga gagacgcaaa aactactcta ttctgtgcat cagatgctaa agcatatgag
181 acagaagtgc ataagtctg ggctacacat gcctgtgtac ccacagacc caaccacaa
241 gaaatagttt tgggaaatgt aacagaaaat ttaatatgt ggaaaaatga catggcagat
301 cagatgcatg aggatgtaat cagtttatgg gatcaaagcc taaagccatg tgtaaagttg
361 accccactct gtgtcacttt aaactgtaca gatacaaatg ttacaggtaa tagaactgtt
421 acaggtataa gtaccaataa tacaatggt acaggtatgt ataacattga agaaatgaaa
481 aattgctctt tcaatgcaac cacagaatta agagataaga aacataaaga gtatgcactc
541 tttatagac ttgatatagt accacttaat gagaatagt acaactttac atatagatta
601 ataaattgca atacctcaac cataacacaa gcctgtccaa aggtctcttt tgaccgatt
661 cctatacatt actgtgtccc agctggttat gcgattctaa agtgaataa taagacattc
721 aatgggacag gaccatgta taatgtcagc acagtacaat gtacacatgg aattaagcca
781 gtggtatcaa ctcaattact gttaaatggt agtctagcag aagaagggat aataattaga
841 tctgaaaatt tgacagagaa taccaaaaca ataatgtac acctaatga atctgtagag
901 attaattgta caagaccaa caataataca agaaaaagt taaggatagg accaggacaa
961 gcattctatg caacaaatga tgtaatagga aacataagac aagcacattg taacattagt
1021 acagatagat ggaacaaaac ttacaacag gtaatgaaaa aattaggaga gcatttcct
1081 aataaaacaa tacaatttaa accacatgca ggaggggac tagaaattac aatgcatagc
1141 ttaattgta gaggagaatt ttctattgt aatacatcaa acctgtttaa tagcacatac
1201 cactctaata atggtacata caaatacaat ggtaattcaa gctcaccat cacactcaa
1261 tgtaaaataa aacaaattgt acgcatgtgg caaggggtag gacaagcaac gtatgcccc
1321 cccattgcag gaaacataac atgtagatca aacatcacag gaatactatt gacacgtgat
1381 ggaggattta acaccacaaa caacacagag acattcagac ctggaggagg agatatgagg
1441 gataactgga gaagtgaatt atataaatat aaagtagtag aaattaagcc attgggaata
1501 gcaccacta aggcaaaaag aagagtgtg cagagagaaa aaagagcagt gggaatagga
1561 gctgtgttcc ttgggttctt gggagcagca ggaagcacta tgggcgcagc gtcaataacg
1621 ctgacggtac aggcagaca actgtgtctt ggtatagtgc aacagcaaag caatttgcgt
1681 aaggctatag aggcgcaaca gcatagttg caactcacag tctggggcat taagcagctc
1741 caggcgagag tcctggctat agaaagatac ctaaaggatc aacagctcct agggatttgg
1801 ggctgctctg gaagactcat ctgcaccact gctgtgcctt ggaactccag ttggagtaat
1861 aaatctgaaa aagatatatt ggataacatg acttggatgc agtgggatag agaaattagt
1921 aattacacag gcttaataa caatttgcct gaagactgcg aaaaccagca ggaaaagaat
1981 gaaaaagatt tattagaatt ggacaagtgg aacaatctgt ggaattggtt tgacatatca
2041 aactggccgt ggtatataaa aatattcata atgatagtag gaggcttgat aggtttaaga
2101 ataattttg ctgtgcttct tatagtgaat agagttaggc agggatactc accttgtca
2161 ttcagaccc ttacccaag cccgagggga ctcgacaggc tcggaggaat cgaagaagaa
2221 ggtggagagc aagacagaga cagatccata cgatttgtga gcgattctt gtcgcttgc
2281 tgggacgac tgcggaacct gtgcctcttc agctaccacc gcttgagaga ctcatatta
2341 attgcagtga gggcagtgga acttctggga cacagcagtc tcaggggact acagaggggg
2401 tgggaaatcc ttaagtatct gggaagtctt gtgcaatatt ggggtctaga gtaaaaaag
2461 agtgctatta gtctgcttga taccatagca ataacagtag ctgaaggaac agataggatt
2521 atagaattag tacaagaat ttgtagagct atcctcaaca tacctagaag aataagacag
2581 ggctttgaag cagctttgct ataa

FIGURE 99

gp140mod.TV1.tpa1 (SEQ ID NO:131)

1 atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt
61 tcgcccagcg ccagcaccga ggacctgtgg gtgaccgtgt actacggcgt gcccggtgg
121 cgcgacgcca agaccacct gtctgcgcc agcgacgcca aggcctacga gaccgaggtg
181 cacaacgtgt gggccacca cgcctgcgtg cccaccgacc ccaaccccca ggagatcgtg
241 ctgggcaacg tgaccgagaa cttcaacatg tggaagaacg acatggccga ccagatgcac
301 gaggacgtga tcagcctgtg ggaccagagc ctgaagccct gcgtgaagct gacccccctg
361 tgcgtgacct tgaactgcac cgacaccaac gtgaccggca accgcaccgt gaccggcaac
421 agcaccaaca acaccaacgg caccggcatc tacaacatcg aggagatgaa gaactgcagc
481 ttcaacgcca ccaccgagct gcgcgacaag aagcacaagg agtacgccct gttctaccgc
541 ctggacatcg tgccctgaa cgagaacagc gacaacttca cctaccgcct gatcaactgc
601 aacaccagca ccatcacca ggctgcccc aaggtgagct tcgaccccat ccccatccac
661 tactgcgcc cgcgggcta cgccatcctg aagtgaaca acaagacctt caacggcacc
721 ggccccctgt acaacgtgag caccgtgcag tgacccacg gcatcaagcc cgtggtgagc
781 acccagctgc tgctgaacgg cagcctggcc gaggagggca tcatcatccg cagcgagaac
841 ctgaccgaga acaccaagac catcatcgtg cacctgaacg agagcgtgga gatcaactgc
901 acccgcccca acaacaacac cgcgaagagc gtgcgcatcg gccccggcca ggcttctac
961 gccaccaacg acgtgatcgg caacatccgc caggccact gcaacatcag caccgaccgc
1021 tggaacaaga cctgcagca ggtgatgaag aagctgggcg agcacttccc caacaagacc
1081 atccagtcca agccccacgc cggcggcgac ctggagatca ccatgcacag cttcaactgc
1141 cgcggcgagt tcttctactg caacaccagc aacctgttca acagcaccta ccacagcaac
1201 aacggcacct acaagtataa cggcaacagc agcagcccca tcacctgca gtgcaagatc
1261 aagcagatcg tgcgcatgtg gcagggcgtg ggccaggcca cctacgcccc cccatcgcc
1321 ggcaacatca cctgccgcag caacatcacc ggcatcctgc tgacccgga cggcggcttc
1381 aacaccacca acaacaccga gacctccgc cccggcggcg gcgacatcg cgacaactgg
1441 cgcagcgagc tgtacaagta caagtggtg gagatcaagc cctggggcat cgccccacc
1501 aaggccaagc gccgcgtggt gcagcgcgag aagcgcgccg tgggcatcgg cgccgtgttc
1561 ctgggcttcc tgggcgccgc cggcagcacc atgggcgccg ccagcatcac cctgaccgtg
1621 caggccccgc agctgctgag cggcatcgtg cagcagcaga gcaacctgct gaaggccatc
1681 gaggccccagc agcatatgct gcagctgacc gtgtggggca tcaagcagct gcaggccccgc
1741 gtgctggcca tcgagcgcta cctgaaggac cagcagctgc tgggcatcgt gggctgcagc
1801 ggccgcctga tctgcaccac cgccgtgccc tggaacagca gctggagcaa caagagcgag
1861 aaggacatct gggacaacat gacctggtg cagtgggacc gcgagatcag caactacacc
1921 ggctgatct acaacctgct ggaggacagc cagaaccagc aggagaagaa cgagaaggac
1981 ctgctggagc tggacaagtg gaacaacctg tggaactggt tcgacatcag caactggccc
2041 tggatcatct aa

FIGURE 100

gp140mod.TV1 (SEQ ID NO:132)

1 gaattcatgc gctgatggg caccagaag aactgccagc agtgggtgat ctggggcatc
 61 ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
 121 ggcggtcccc tgtggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgccac cgacccaac
 241 cccaggaga tcgtgctggg caacgtgacc gagaactca acatgtggaa gaacgacatg
 301 gccgaccaga tgcagagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgaccc cctgtgctg gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag
 481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtac
 541 gccctgttct accgctgga catcgtcccc ctgaacgaga acagcgacaa ctacacctac
 601 cgcctgatca actgcaacac cagcaccatc acccaggcct gcccgaagg gagcttcgac
 661 cccatcccca tccactactg cgccccgcc ggctacgcca tctgaagt caacaacaag
 721 acctcaacg gcaccggccc ctgtacaaac gtgagcaccg tgcagtgcac ccacggcatc
 781 aagcccgtgg tgagcaccga gctgctgctg aacggcagcc tggccgagga gggcatcatc
 841 atcgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
 901 gtggagatca actgcaccg cccaacaac aacaccgca agagcgtgcg catcgcccc
 961 ggccaggcct tctacgccac caacgacgtg atcggaaca tccgccaggc cactgcaac
 1021 atcagcaccg accgtggaa caagaccctg cagcaggtga tgaagaagct gggcgagcac
 1081 tccccaaaca agaccatcca gttaagccc cagcgcggcg gcgacctgga gatcaccatg
 1141 cacagttca actgcgcgg cgagttctt tactgaaca ccagcaacct gttaacagc
 1201 acctaccaca gcaacaacgg cactacaag tacaacggca acagcagcag cccatcacc
 1261 ctgcagtga agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
 1321 gccccccca tcgccggcaa catcacctgc cgcagcaaca tcaccggcat cctgtgacc
 1381 cgcgacggcg gttcaacac caccaacaac accgagacct tccgccccgg cggcgcgac
 1441 atcgcgcaca actggcgag cgagctgtac aagtacaagg tgggtggagat caagcccctg
 1501 ggcatgccc ccaccaaggc caagcgcgc gtggtgcagc gcgagaagcg cgccgtgggc
 1561 atcggcgccg tgttctggg ctctctgggc gccgcccga gcacatggg cgcgcccagc
 1621 atcacctga cgtgcaggc ccgcagctg ctgagcggca tcgtgcagca gcagagcaac
 1681 ctgtgaagg ccatcgagg ccagcagcac atgtgcagc tgaccgtgtg gggcatcaag
 1741 cagctgcagg cccgcgtgct ggcatcgag cgctacctga aggaccagca gctgctgggc
 1801 atctggggct gcagcggccg cctgatctgc accaccgccc tgcctggaa cagcagctgg
 1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
 1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
 1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtggaa ctggttcgac
 2041 atcagcaact ggccctggta catctaactc gag

FIGURE 101

gp140mod.TV1.wtLnative (SEQ ID NO:133)

1 gaattcatga gagtgatggg gacacagaag aattgtcaac aatggtggat atggggcatc
61 ttaggcttct ggatgctaata gatttgaac accgaggacc tgtgggtgac cgtgtactac
121 ggcggtgccc tgtggcgcca cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgcccac cgacccaac
241 cccagaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgacc cctgtgcgt gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcactacaa catcgaggag
481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtag
541 gccctgttct accgcttga catcgtgccc ctgaacgaga acagcgacaa cttcacctac
601 cgcctgatca actgcaacac cagcaccatc acccaggcct gcccgaagg gagcttcgac
661 cccatcccca tccactactg cgccccgcc ggctacgcca tctgaagtg caacaacaag
721 accttcaacg gcaccggccc ctgctacaac gtgagcaccg tcagtgacac ccacggcatc
781 aagcccgtgg tgagcaccca gctgctgctg aacggcagcc tggccgagga gggcatcatc
841 atccgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
901 gtggagatca actgcaccg cccaacaac aacaccgcga agagcgtgcg catcgcccc
961 ggccaggcct tctacgccac caacgacgtg atcggcaaca tccgccaggc cactgcaac
1021 atcagcaccg accgctggaa caagacctg cagcaggtga tgaagaagct gggcgagcac
1081 tccccaca agaccatcca gttcaagccc cagccggcg gcgacctgga gatcaccatg
1141 cacagttca actgccgcg cgagttctc tactgcaaca ccagcaacct gttcaacagc
1201 acctaccaca gcaacaacg cacctacaag tacaacggca acagcagcag cccatcac
1261 ctgcagtga agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
1321 gccccccca tcgccggcaa catcacctgc cgcagcaaca tcaccggcat cctgctgacc
1381 cgcgacggcg gttcaacac caccaacaac accgagacct tccgccccg cgcgggcgac
1441 atgcgcgaca actggcgag cgagctgtac aagtacaagg tggaggagat caagccctg
1501 ggcacgccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg cgccgtgggc
1561 atcgcgccg tgttctggg cttcctggg gccgccggca gcacatggg cgccgccagc
1621 atcacctga cgtgcagcg ccgccagctg ctgagcggca tcgtgcagca gcagagcaac
1681 ctgctgaagg ccatcgaggc ccagcagcac atgtgcagc tgaccgtgtg gggcatcaag
1741 cagctgcagg cccgctgct ggccatcgag cgctacctga aggaccagca gctgctgggc
1801 atctggggct gcagcggcg cctgatctgc accaccgccc tgccctggaa cagcagctgg
1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtggaa ctggttcgac
2041 atcagcaact ggccctggtg catctaactc gag

FIGURE 102

NefD125G_TV2_C_ZAopt (SEQ ID NO:134)

ATGGGCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC
GAGCGCATCCGCCGCACCCGCAGCGCCGCCGAGGGCGTGGGCAGCGCCAGC
CAGGACCTGGAGAAGCACGGCGCCCTGACCACCAGCAACACCGCCCACAAC
AACGCCGCCTGCGCCTGGCTGGAGGCCCAGGAGGAGGAGGGCGAGGTGGGC
TTCCCCGTGCGCCCCCAGGTGCCCCTGCGCCCCATGACCTACAAGGCCGCCAT
CGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCAAGAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC
TTCTTCCCCGGCTGGCAGAACTACACCCCCGGCCCCGGCGTGCGCTTCCCCCT
GACCTTCGGCTGGTACTTCAAGCTGGAGCCCGTGGACCCCCGCGAGGTGGAG
GAGGCCAACGAGGGCGAGAACAACCTGCCTGCTGCACCCCATGAGCCAGCAC
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTTCGACAGCACC
CTGGCCCGCCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACT
GCTGA

FIGURE 103

105040-52566860

NefD125G-Myr_TV2_C_ZAopt (SEQ ID NO:135)

ATGGCCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC
GAGCGCATCCGCCGCACCCGCAGCGCCGCCGAGGGCGTGGGCAGCGCCAGC
CAGGACCTGGAGAAGCACGGCGCCCTGACCACCAGCAACACCGCCCCACAAC
AACGCCGCCTGCGCCTGGCTGGAGGCCCAGGAGGAGGAGGGCGAGGTGGGC
TTCCCCGTGCGCCCCCAGGTGCCCTGCGCCCCATGACCTACAAGGCCGCCAT
CGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCAAGAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC
TTCTTCCCCGGCTGGCAGAACTACACCCCGGCCCGGCGTGCGCTTCCCCCT
GACCTTCGGCTGGTACTTCAAGCTGGAGCCCGTGGACCCCGCGAGGTGGAG
GAGGCCAACGAGGGCGGAGAACAACCTGCCTGCTGCACCCCATGAGCCAGCAC
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTTCGACAGCACC
CTGGCCCGCCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACT
GCTGA

FIGURE 104

106040" 52565360

↓: is the regions for β -sheet deletions

*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N \rightarrow Q) or deletions can be performed.

		1		50
SF162	(1)	----MDAMKRG	LLCCVLL	CGAVFVSPSAVEK
TV1.8_2	(1)	MRVMGTQKNC	QQWWIWGILG	FWMLMICNTEDL
TV1.8_5	(1)	MRVMGTQKNC	QQWWIWGILG	FWMLMICNTEDL
TV2.12-5/1	(1)	MRARGILKNY	RHWWIWGILG	FWMLMNCNVKGL
Consensus	(1)	MRVMGTQKNC	QQWWIWGILG	FWMLMICNVEDL
		51		100
SF162	(47)	FCASDAKAYD	TEVHNWATHAC	VPDNPQEI
TV1.8_2	(51)	FCASDAKAYE	TEVHNWATHAC	VPDNPQEI
TV1.8_5	(51)	FCASDAKAYE	TEVHNWATHAC	VPDNPQEI
TV2.12-5/1	(51)	FCASDAKAYE	KEVHNWATHAC	VPDNPQEI
Consensus	(51)	FCASDAKAYE	TEVHNWATHAC	VPDNPQEI
		101		150
			$\beta 2 / V 1 V 2 / \beta 3$	*
SF162	(97)	QMHE	DIISLWDQSLKPCVKLTPLCVTLHCTNLK	NATNTK-----SSN---
TV1.8_2	(101)	QMHE	DVLSLWDQSLKPCVKLTPLCGVTLNCTD	TNVTGNRTVTGNSTNTNNG
TV1.8_5	(101)	QMHE	DIISLWDQSLKPCVKLTPLCGVTLNCTD	TNVTGNRTVTGNNDTNIA
TV2.12-5/1	(101)	QMQED	IISLWDQSLKPCVKLTPLCVTLNCTNAT	VNYN-----NTS---
Consensus	(101)	QMHE	DIISLWDQSLKPCVKLTPLCVTLNCTN	TNVTGNRTVTGNSNSN A
		151		*200
SF162	(139)	WKEMDRGEI	KNCSEKVTTSIRNKM	QKEYALFYKLDVVPIDN----DNTSY
TV1.8_2	(151)	TGIYNI	BEEMKNCSEFNATTEL	RDKKHKEYALFYRLDIVPLN--ENS
TV1.8_5	(151)	NATYKY	BEEMKNCSEFNATTEL	RDKKHKEYALFYKLDIVPLN--ENS
TV2.12-5/1	(141)	-----	KDMKNCSEFYVTTEL	RDKKKKENALFYRLDIVPLNNRKN
Consensus	(151)	A Y	BEEMKNCSEFNVTTEL	RDKKHKEYALFYKLDIVPLNN ENS
		201		*250
SF162	(185)	KLINCNTSV	ITOACPKVSFEP	PIPIHYCAPAGFAILKCNDKKFNGSG
TV1.8_2	(199)	RLINCNTST	ITOACPKVSFD	PIPIHYCAPAGYAILKCNNKTFNGT
TV1.8_5	(199)	RLINCNTST	ITOACPKVSFD	PIPIHYCAPADYAILKCNNKTFNGT
TV2.12-5/1	(185)	RLINCNTSA	ITTOACPKVSFD	PIPIHYCAPAGYAPLKCNNKKFNGIG
Consensus	(201)	RLINCNTST	ITOACPKVSFD	PIPIHYCAPAGYAILKCNNKTFNGT
		251		*300
SF162	(235)	VSTVQCTH	GIRPVVSTQLL	NGSLAEEGVVIRSENFTDNAKTIIV
TV1.8_2	(249)	VSTVQCTH	GIRPVVSTQLL	NGSLAEEGIIIRSENLTENTKTIIV
TV1.8_5	(249)	VSTVQCTH	GIRPVVSTQLL	NGSLAEEGIIIRSENLTENTKTIIV
TV2.12-5/1	(235)	VSTVQCTH	GIRPVVSTQLL	NGSLAEEIIIRSENLTNNVKTIIIV
Consensus	(251)	VSTVQCTH	GIRPVVSTQLL	NGSLAEEGIIIRSENLTENTKTIIV
		301*		*350
SF162	(285)	VEINCTRP	NNNTRKSIITIG	PGRAFATGDIIGDITROAHCNIS
TV1.8_2	(299)	VEINCTRP	NNNTRKSVRIG	PGQAFYATNDVIGNTROAHCNIST
TV1.8_5	(299)	VEINCTRP	NNNTRKSVRIG	PGQAFYATNDVIGNTROAHCNIST
TV2.12-5/1	(285)	IEIKCTRP	GNNNTRKSVRIG	PGQAFYATGDIIGDITROAHCNIS
Consensus	(301)	VEINCTRP	NNNTRKSVRIG	PGQAFYATNDIIGNITROAHCNIST

FIGURE 105A

		351	*		*	400	*
SF162	(335)	KQIVTKLQAQFGNKT-	IVFKQSSGGDPEI	VMHSFNCGGEFFYC	NSTQLFN		
TV1.8_2	(349)	QQVMKKLGEHFPNKT-	IOFKPHAGGDLEIT	MHSFNCRGEEFYCN	TSNLFN		
TV1.8_5	(349)	QQVMKKLGEHFPNKT-	IKFEPHAGGDLEIT	MHSFNCRGEEFYCN	TSNLFN		
TV2.12-5/1	(335)	QRVSQKLQELFPNST	GIKFAPHSGGDLEI	TTHSFNCGGEEFYCN	TTDLFN		
Consensus	(351)	QQVMKKLQEHFPNKT	IKFKPHAGGDLEIT	MHSFNCRGEEFYCN	TSNLFN		
		401	*	*		450	
					β20/β21		
SF162	(384)	STWNN-----	TIGPN-NTNGTITL	PCRIKQIINRWQEV	GKAMYAPPIRG		
TV1.8_2	(398)	STYHS---	NNGTYKNGNSSSPIT	LQCKIKQIVRMWQV	GQATYAPPIAG		
TV1.8_5	(398)	STYYP---	KNGTYKNGNSSLPIT	LQCKIKQIVRMWQV	GQAMYAPPIAG		
TV2.12-5/1	(385)	STYSNGTCTNCT	CMSEN--NTERITLQ	CRKQIINMWQEV	GRAMYAPPIAG		
Consensus	(401)	STYHN	NGTYKNGNSS	PITLQCKIKQIIR	MWQVGQAMYAPPIAG		
			*				
		451	*	*	*	500	
SF162	(427)	QIRCSSNITGILL	TRDGGKEISNT--	TEIFRPGGGDMRD	NWRSELYKYKV		
TV1.8_2	(445)	NITCRSNITGILL	TRDGGFNNTNN--	TETFRPGGGDMRD	NWRSELYKYKV		
TV1.8_5	(445)	NITCRSNITGILL	TRDGGFNNTNND	TEETFRPGGGDMRD	NWRSELYKYKV		
TV2.12-5/1	(433)	NITCRSNITGILL	TRDGGDNNTET--	ETFRPGGGDMRD	NWRSELYKYKV		
Consensus	(451)	NITCRSNITGILL	TRDGGFNNTNT	TETFRPGGGDMRD	NWRSELYKYKV		
		501				550	
SF162	(475)	VKIEPLGVAPT	KAKRRVVQREKRA	VTLGAMFLGFLGA	AGSTMGARSLT	LT	
TV1.8_2	(493)	VEIKPLGIAPT	KAKRRVVQREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
TV1.8_5	(495)	VEIKPLGIAPT	KAKRRVVQREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
TV2.12-5/1	(480)	VEIKPLGVAPT	AAKRRVVEREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
Consensus	(501)	VEIKPLGIAPT	KAKRRVVQREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
		551				600	
SF162	(525)	VQARQLLSGIV	QQQNNLLRAIEA	QOHLLOLTVWGI	KQLOARVLA	VERYLK	
TV1.8_2	(543)	VQARQLLSGIV	QQQSNLLKATEA	QOHLLOLTVWGI	KQLOARVLA	IERYLK	
TV1.8_5	(545)	VQARQLLSGIV	QQQSNLLKATEA	QOHLLOLTVWGI	KQLOARVLA	IERYLK	
TV2.12-5/1	(530)	VQARQLLSGIV	QQQSNLLRAIEA	QOHLLOLTVWGI	KQLOARVLA	IERYLK	
Consensus	(551)	VQARQLLSGIV	QQQSNLLKATEA	QOHLLOLTVWGI	KQLOARVLA	IERYLK	
							*
		601		*	*	650	
SF162	(575)	DQQLLGIWGC	SGKLICTTAVP	WNASWSNKS	LDQIWNMTW	MEWEREIDNY	
TV1.8_2	(593)	DQQLLGIWGC	SGRLICTTAVP	WNSSWSNK	SEKDIWDN	MTWMQWDREISNY	
TV1.8_5	(595)	DQQLLGIWGC	SGRLICTTAVP	WNSSWSNK	SEADIWDN	MTWMQWDREINNY	
TV2.12-5/1	(580)	DQQLLGIWGC	SGKLICTTNVL	WNSSWSNK	TOSDIWDN	MTWMQWDREISNY	
Consensus	(601)	DQQLLGIWGC	SGKLICTTAVP	WNSSWSNK	SEADIWDN	MTWMQWDREISNY	
		651				700	
SF162	(625)	TNLIYTLIEES	QNQOEKNEQELLE	LDKWLWNW	FDISKWLWYIKIF	IMI	
TV1.8_2	(643)	TGLIYNLLED	SQNQOEKNEKDLLE	LDKWNNLWN	WFDISNWPWYIKIF	IMI	
TV1.8_5	(645)	TETIFRLLED	SQNQOEKNEKDLLE	LDKWNNLWN	WFDISNWLWYIKIF	IMI	
TV2.12-5/1	(630)	TNTIYRLLED	SQSQOEKNEKDL	LALDRWNNLWN	WFSITNWLWYIKIF	IMI	
Consensus	(651)	TNTIYRLLED	SQNQOEKNEKDLLE	LDKWNNLWN	WFDISNWLWYIKIF	IMI	
		701				750	
SF162	(675)	VGGLVGLRIV	FTVLSIVNRV	ROGYSPLSFQ	TRFPAPRGP	DRPEGIEEEGG	
TV1.8_2	(693)	VGGLIGLRII	FAVLSIVNRV	ROGYSPLSFQ	TLTPSPRGL	DRLGIEEEGG	
TV1.8_5	(695)	VGGLIGLRII	FAVLSIVNRV	ROGYSPLSFQ	TLTPSPRGL	DRLGIEEEGG	
TV2.12-5/1	(680)	VGGLIGLRII	FAVLSIVNRV	ROGYSPLSLQ	TLIPNPRGP	DRLGIEEEGG	
Consensus	(701)	VGGLIGLRII	FAVLSIVNRV	ROGYSPLSFQ	TLTPSPRGP	DRLGIEEEGG	

FIGURE 105B

		751	800
SF162	(725)	ERDRDRSSPLVHGLLALIWDLLRSICLFSYHRLRDLILIAARIVELLGR-	
TV1.8_2	(743)	EQDRDRSIRLVSGFLSLAWDDLRLNLCFSYHRLRDFILIAVRAVELLGHS	
TV1.8_5	(745)	EQDRDRSIRIVSGFLSLAWDDLRSICLFSYHRLRDFILIAVRAVELLGHS	
TV2.12-5/1	(730)	EQDSSRSIRLVSGFLTLAWDDLRSICLFCYHRLRDFILIVVRAVELLGHS	
Consensus	(751)	EQDRDRSIRLVSGFLSLAWDDLRLNLCFSYHRLRDFILIAVRAVELLGHS	
		801	850
SF162	(774)	-----RGWEALKYWGNNLOYWIOELKNSAVSLFDAIAIAVAEGTDRIIE	
TV1.8_2	(793)	SLRGLQRGWEILKYLGLSVQYWGLELKKSALSLDITIAITVAEGTDRIIE	
TV1.8_5	(795)	SLRGLQRGWEILKYLGLSVQYWGLELKKSALSPDITIAIAVAEGTDRIIE	
TV2.12-5/1	(780)	SLRGLQRGWGTLKYLGLSVQYWGLELKKSALNLLDITIAIAVAEGTDRIIE	
Consensus	(801)	SLRGLQRGWEILKYLGLSVQYWGLELKKSALSLDITIAIAVAEGTDRIIE	
		851	876
SF162	(818)	VAQRIGRAFLHIPRRIRQGFERALL-	
TV1.8_2	(843)	LVQRICRAILNIPRRIRQGFEEAALL-	
TV1.8_5	(845)	LVQRICRAILNIPRRIRQGFEEAALL-	
TV2.12-5/1	(830)	FIONLCRGIRNVPRRIRQGFEEAALQ-	
Consensus	(851)	LVQRICRAILNIPRRIRQGFEEAALL	

FIGURE 105C